us-09-698-903b-12.rnpb

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December 5, 2004, 06:58:29; Search time 16.704 Seconds (without alignments) 6907.991 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                        OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	sult No.	Score		Query Match Length DB ID	DB	ΩI	Description
		19.4	!	21		US-09-733-151-12	Sequence 12, Appl
	N	19.4	92.4		15	US-10-375-332-12	Sequence 12, Appl
U	m	19.4		694	6	US-09-733-151-39	Sequence 39, Appl
υ	4	19.4			15	US-10-375-332-39	Sequence 39, Appl
	S	19.4			σ	US-09-794-384A-7	Sequence 7, Appli
	9	19.4			17	US-10-801-550-7	Sequence 7, Appli
υ	7	19.4			σı	US-09-733-151-36	Sequence 36, Appl
U	ω	19.4				US-10-375-332-36	Sequence 36, Appl
U	σ	19.4	92.4	1077	σ	US-09-733-151-24	Sequence 24, Appl
υ	10	19.4		_	15	US-10-375-332-24	Sequence 24, Appl
	11	19.4		۷.	13	US-10-047-542-13	Sequence 13, Appl
υ	12	19.4		4.	თ	US-09-733-151-2	Sequence 2, Appli

Sequence 2, Appli	,	Sequence 1,	equence 7,	e v	equence 4,	g G	_	o o	a)	Sequence 1	equence 4,	4	(L)	a)	a)	• •	ednence ;	ednence ;	٠.	٠.	a)	4	0)	•		٠.		equence	ednence		Sequence 25, Appl	Seguence 28, Appl	
0-375-	-733-151	0-375-33	-970-92	-509-94	-509-94	US-10-047-542-100	US-10-047-542-101	Ξ		US-10-047-542-14	US-09-847-057-4	US-09-874-926-4	US-09-940-550A-11	US-10-033-190-3	US-09-792-568-8	US-10-250-821-22	US-10-250-553-22	1-2	US-10-250-553-21	US-10-250-821-20	3-2	US-09-948-138-4	US-10-033-190-5	ĕ	US-09-792-568-9	L	3-2	1-2	3-2	1-2) 16 US-10-250-553-25	1-2	
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92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	
19.4	19.4	19.4	19.4	19.4	. 7.	19.4	19.4	٠.	19.4	٠.	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4	19.4		19.4			19.4		
13	14	15	16	17	8	6	20	21	22	23	24	25	56	27	28	59	30	31	3.2	33	34	5	36	3.7	38	3	40	41	42	4 1	44	45	
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ALIGNMENTS

JS-09-733-151-12

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USE OF 19-13-15-12.

USE OF 19-13-15-12.

USE OF OR APPLICATION US/0973151

PATENT NO. US2001002962041

PATENT NO. US2001002962041

PATENTINE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME

PILE REFERENCE: 514412-2019

CURRENT PELLOATION NUMBER: US/09/733,151

CURRENT PELLING DATE: 2000-12-08

PRIOR PELLING DATE: 1999-12-08

PRIOR PILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: PATENTIN VERSION 3.0

SOFTWARE: ALIGICAL SEQUENCE

FRATURE: IN O12

LENGTH: 21

CRANICK: ALIGICAL SEQUENCE

FRATURE: LOCATION: (1)...(21)

LOCATION: (1)...(21)

US-09-733-151-12
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RESULT 2 US-10-375-332-12

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NAME/KEY: misc feature
LOCATION: (1)..[(694)
OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09794384A

Sequence 7, Application US/09794384A

Petent No. US20020144305A1

SEQUENCE 1 NO. US20020144305A1

APPLICANT: Dellaporta, Stephen L.

APPLICANT: Moreno, Maria A.

APPLICANT: Moreno, Maria A.

TITLE OF INVENTION: Transmission of a Transgene

TITLE OF INVENTION: Transmission of a Transgene

TITLE OF INVENTION: Transmission of a Transgene

TITLE OF INVENTION: WINDER: US/09/794,384A

CURRENT APPLICATION NUMBER: US/09/794,384A

CURRENT FILING DATE: 2001-02-28

PRIOR PILING DATE: 2000-02-28

PRIOR PILING DATE: 2000-02-28

WINDER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Moreno, Maria A.
APPLICANT: Moreno, Maria A.
APPLICANT: Yale University
TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
TITLE OF INVENTION: Transmission of a Transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Length 831;
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92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
                              CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GCTTGGACTATAATACTTGAC 21
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             FILE REFERENCE: 514412-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: polyA_signal
; LOCATION: (514)..(813)
US-09-794-384A-7
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LENGTH: 831
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                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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OTHER INFORMATION: sequence comprising the 5' flanking region of RF-EN1 in WOSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
                                                                        APPLICANT: De Both, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
CURRENT APPLICATION NUMBER: US/10/375,332
FRIOR FILING DATE: 2003-02-27
FRIOR FILING DATE: 2000-12-08
FRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VERSION 3.0
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TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
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92.4%; Score 19.4; DB 15; Length 21;
Best Local Similarity 95.2%; Pred. No. 5.7;
Matches 20; Conservative 0; Mismatches 1; Indels
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92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LOCATION: (1). (21)
; OTHER INFORMATION: primer 201(BNA01)
US-10-375-332-12
Sequence 12, Application US/10375332
Publication No. US20030188347A1
GENERAL INFORMATION:
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US-09-733-151-39/c
; Sequence 39, Application US/09733151
; Patent No. US2001002620A1
; GENERAL INFORMATION:
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Publication No. US20030188347A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(694)
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LENGTH: 694
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LENGTH: 21
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US-10-375-332-24/c

US-10-375-332-24/c

US-10-375-332-24/c

US-20-375-332-24/c

USEQUENCE 24, Application US/10375332

EDUBLICALION NO. US20030188347A1

GENERAL INFORMATION:

TITLE OF INVENTION: HYBRID WINTER DILEED RAPE AND METHODS FOR PRODUCING SAME

FILE REFERENCE: 514412-2019

CURRENT PILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: US/09/733,151

PRIOR PELING DATE: 1999-12-08

PRIOR PILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFITABLE: Patentin version 3.0

SEQ ID NO 24

LENGTH: 1077
                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
COCATION: (1)...(909)
US-10-375-332-36
US-10-375-332-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MS-09-73-151-24/C

Sequence 24, Application US/09733151

Sequence 24, Application US/09733151

Sequence 24, Application US/09733151

Sequence 24, Application US/09733151

Sequence 24, Application US/090620A1

PRESENTATION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME TITLE OF INVERTION: HYBRID WINTER: US/09/733,151

CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT FILING DATE: 09/457,037

PRIOR APPLICATION NUMBER: 09/457,037

PRIOR APPLICATION NUMBER: 09/457,037

PRIOR PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 24

LENGTH: 1077
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ORGANISM: Brassica napus
FEATURE:
MAME/KET: misc feature
LOCATION: (1). (1077)
OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                  Query Match
92.4%; Score 19.4, I
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
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PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 909
LENGTH: 909
TYPE: DNA
ORGANISM: Artificall sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: De Both, et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SSOFTWARE: Patentin version 3.0
SEQ ID NO 36
LENGTH: 909
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Sequence 36, Application US/10375332
Sequence 36, Application US/10375332
Publication No. USZ0030188347A1
Publication No. USZ0030188347A1

APPLICANT: De Both, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME TILE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION WHERE: US/09/733,151
PRIOR APPLICATION NUMBER: 09/457,037
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92.4%; Score 19.4; DB 9; Length 909;
Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 95.2%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches
  FILE REFERENCE: 44574-5078-US
CURRENT APPLICATION NUMBER: US/10/801,550
CURRENT FILING DATE: 2004-03-17
PRIOR APPLICATION NUMBER: US/09/794,384
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 831
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                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 dcircaichararachad 684
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Patent No. US20010029620A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificail sequence
                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: polyA signal
; LOCATION: (514)..(813)
US-10-801-550-7
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US-09-733-151-1/c
                                SOFTWARE:
SEQ ID NO 2
LENGTH: 483
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| Sequence 13, Application US/20020168367A1
| GENERAL INFORMATION:
| APPLICANT: LARRICK, JAMES W.
| APPLICANT: WYCOFF, KEITH L.
| TITLE OF INVENTION: NOVEL INVUNCAPHESINS FOR TREATING AND PREVENTING VIRAL
| TITLE OF INVENTION: AND BACTERIAL DISEASES
| FILE REFERENCE: 030905,0004.CIP1
| CURRENT APPLICATION NUMBER: US/10/047,542
| CURRENT PILING DATE: 2001-04-28
| PRIOR FILING DATE: 2001-04-28
| PRIOR FILING DATE: 2000-04-28
| REOR FAPLICATION NUMBER: 60/200,298
| PRIOR FILING DATE: 2000-04-28
| NUMBER OF SEQ ID NOS: 101
| SOFTWARE: Patentin Ver. 2.1
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Barent No. US20010029620A1

GENERAL INFORMATION:
APPLICANT: De Both, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
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                                                                     ; NAME/KEY: misc_feature
; DCATTON: (1)...(1077)
; OTHER INCOMMATION: sequence comprising the 5' flanking region of MS-BN1
US-10-375-332-24
                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                            Length 1077;
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                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSP-1
                                                                                                                                                                                          DB 15;
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92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches
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1 LOCATION: (2214)..(2215)
1 OTHER INFORMATION: a, c, t or g
US-10-047-542-13
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NAME/KEY: modified base
LOCATION: (2150)
OTHER INFORMATION: a, c, t
TYPE: DNA
ORGANISM: Brassica napus
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US-10-047-542-13
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LENGTH: 4465
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APPLICANT: De Boch, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
CURRENT APPLICATION NUMBER: 2009-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: De BOCH, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TILLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR FILING DATE: 2000-12-08
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTION NOS: 43
LENGTH: 4832
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92.4%; Score 19.4; D
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GCTTGGACTATAATACCTGAC 143
                                                                                                                                                                                   ) NAME/KEY: misc_feature

) LOCATION: (1)..(4832)

; OTHER INFORMATION: Plasmid pTHW118

US-09-733-151-2
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; LOCATION: (1)..(4832)
; OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2
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Publication No. US20030188347A1
GENERAL INFORMATION:
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Patent No. US20010029620A1
GENERAL INFORMATION:
                              PatentIn version 3.0
                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS:
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US-10-375-332-2/c
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ORGANISM: Artificial Sequence

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RESULT 15
US-10-375-332-1/c

JUS-10-375-332-1/c

Sequence 1, Application US/10375332

Publication No. UG20030188347A1

GENERAL INFORMATION:

APPLICANT: De Boch,

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME;

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME;

TITLE OF INVENTION NUMBER: US/09/733,151

PRIOR PLILING DATE: 2003-02-27

PRIOR PLILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTIN NUMBER: 09/457,037

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 1

LENGTH: 4946
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92.4%; Score 19.4; DB 15; Length 4946;
Best Local Similarity 95.2%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                               Query Match 92.4%; Score 19.4; DB 9; Length 4946; Best Local Similarity 95.2%; Pred. No. 15; Matches 20; Conservative 0; Mismatches 1; Indels 0
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NAME/KEY: misc_feature
LOCATION: [1]...(4946)
OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1
FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(4946)

OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                 1 GCTTGGACTATATACTTGAC 21
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ORGANISM: Artificial Sequence
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                                                                                                      December 5, 2004, 05:20:20; Search time 3.528 Seconds (without alignments) 4230.886 Million cell updates/sec
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Sequence 2
Sequence 2
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-457-037B-12
US-09-430-497A-8
US-09-430-497A-8
US-09-430-497A-10
US-09-733-151-39
US-09-733-151-39
US-09-733-151-39
US-09-733-151-36
US-09-733-151-36
US-09-457-037B-24
US-09-457-037B-24
US-09-457-037B-24
US-08-64-121-2
US-08-64-440-2
US-09-084-889-2
US-09-084-889-2
US-09-084-889-2
US-09-084-889-2
US-09-084-889-3
US-09-084-88-03-3
US-09-084-88-03-3
US-09-084-88-03-3
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US-09-086-625-3
US-09-64-88-03-3
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S-08-694-824-23
S-08-694-824-22
S-08-694-824-22
S-09-695-782-2
S-09-695-782-2
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Maximum Match 100%
Listing first 45 summaries
                                                                      nucleic search, using sw model
                                                                                                                                                                                                                   1 gcttggactataatacttgac 21
                                                                                                                                                                                                                                                   IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                           US-09-698-903B-12
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                            Run on:
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No.
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US-09-457-037B-12

Sequence 12, Application US/09457037B

Sequence 12, Application US/09457037B

Sequence 12, Application US/09457037B

Sequence 12, Application US/09457037B

GENERAL INFORMATION:

TITLE OF INVENTION: HYBERD WINTER CILSEED RAPE AND METHODS FOR PRODUCING SAME

TILE REFERENCE: 514412-2019

CURRENT APPLICATION NUMBER: US/09/457,037B

CURRENT PILING DATE: 1999-12-08

FRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 21

LENGTH: 21

TYPE: DNA

CURRENT SATURE: Artificial Sequence

FEATURE:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-430-497A-12
US-09-430-497A-12
US-09-430-497A-12

Sequence 12, Application US/09430497A

Sequence 12, Application US/09430497A

Sequence 12, INPORATION:

JEAUREL INFORMATION:

APPLICANT: DE BEUCKELEER, Marc

APPLICANT: DE BEUCKELEER, Marc

TITLE OF INVENTION: BALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING

TITLE OF INVENTION: BALE

FILE REFERENCE: 514412-2020

CURRENT FILING DAME: 1999-10-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

LENGTH: 21
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                                                                                    Sequence
Seq
                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: MDB201
US-09-430-497A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 21; Conservative 0; Mismatches 0; Indels
                       US-09-080-625-4
US-09-457-031-2
US-09-457-031-2
US-09-433-151-2
US-09-437-131-1
US-09-437-151-1
US-09-733-151-1
US-09-733-151-1
US-09-743-151-1
US-09-743-151-1
US-09-817-188-5
US-08-817-188-5
US-08-817-188-5
US-08-458-093-4
US-09-458-093-4
US-09-458-093-4
US-09-430-447A-1
US-09-430-447A-1
US-09-430-447A-1
US-09-430-447A-1
US-09-430-447A-1
US-09-430-447A-1
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. LOCATION: (1). 7(694)
. OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1 in WOSR
US-09-457-037B-39
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Sequence 39, Application US/09457037B

Facent No. 5560963

GRENAL INFORMATION: 
APPLICANT: DE BOth, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B

CURRENT APPLICATION NUMBER: 09/457,037

FRICK APPLICANTON TOWNER: 09/457,037

SROF RILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin version 3.0

SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BENCKELBER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REPRENCE: 514412-2020
CUBRENT PILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                       Gaps
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GRGANISM: Artificial Sequence
FEATURE:
GOTHER INFORMATION: Description of Artificial Sequence: 3' border
GOTHER INFORMATION: flanking region of elite event MS-B2
MANE/KET: misc feature
GOTHER INFORMATION: T-DNA
MANE/KET: misc feature
LOCATION: (1)-(193)
GOTHER INFORMATION: T-DNA
MANE/KET: misc feature
LOCATION: (194)...(416)
GOTHER INFORMATION: plant DNA
US-09-430-497A-10
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                                                                                 Query Match 92.4%; Score 19.4; DB 4; Length 415; Best Local Similarity 95.2%; Pred. No. 0.9; Matches 20; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09430497A Patent No. 6509516
                                                                                                                                                                                                                                       335 GCTTGGACTATAATACCTGAC 315
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  ; OTHER INFORMATION: T-DNA US-09-430-497A-8
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APPLICANT: De Both, et al.
APPLICANT: De Both, et al.
TITLE OF INVENTION: HERBID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43.
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 21
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APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REPERENCE: 514412_2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
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NAME/KEY: misc_feature
LOCATION: (1)...(234)
OTHER INFORMATION: plant DNA
NAME/KEY: misc_feature
LOCATION: (235)...(415)
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                                                                                                                          Query Match 92.4%; Score 19.4; DB 4; Length 21; Best Local Similarity 95.2%; Pred. No. 0.66; Matches 20; Conservative 0; Mismatches 1; Indels
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          LOCATION: (1). (21)
COTHER INFORMATION: primer 201(BNA01)
US-09-457-037B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: primer 201 (BNA01) US-09-733-151-12
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US-09-733-151-12
Sequence 12, Application US/09733151
; Patent No. 6563026
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ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
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RESULT 9
US-09-457-037B-36/c

| Sequence 36, Application US/09457037B
| Patent No. 6506563
| GENERAL INFORMATION:
| APPLICANT: DE BOth, et al.
| TITLE OF INFORMATION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
| CURRENT FILING DATE: 2004-12-08
| PRIOR PAPLICATION NUMBER: 09/457,037
| PRIOR PELING DATE: 1999-12-08
| WINDER OF SEQ ID NOS: 44
| SEQ ID NO 36
| LENGTH: 909
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NAME/KEY: misc_feature
LOCATION: (1)...(909)
LOCATION: (1)...(909)
CTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 in WOSR
US-09-733-151-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/09733151
Sequence 36, Application US/09733151
Patent No. 6563026
PREMATION:
APPLICANT:
APPLICANT:
APPLICANTION:
TILLE OF INVENTION:
FILE REFERENCE: 514412-2019
CURRENT FILING DATE: 2000-12-08
FURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
LINGTH: 909
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SOGANISM: Artificial sequence

PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(909)

JOCATION: (1)...(909)

US-09-457-037B-36

US-09-457-037B-36
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92.4%; Score 19.4; DB 4; Length 909;
Best Local Similarity 95.2%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 1; Indels
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                                                           664 GCTTGGACTATAATACCTGAC 684
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21
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US-09-457-037B-24/c
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US-09-794-384A-7

is Sequence 7, Application US/09794384A

is parent No. 6743968

j GENERAL INFORMATION:
 j APPLICANT: Dellaporta, Stephen L.
 APPLICANT: Moreno, Maria A.
 j APPLICANT: Yale University
 TITLE OF INVENTION: Transmission of a Transgene
 TITLE OF INVENTION: Transmission of a Transgene
 FILE REFERENCE: 44574-5078-028
 CURRENT FILING DATE: 2001-02-28
 PRIOR FILING DATE: 2000-02-28
 NUMBER: OF SEQ ID NOS: 16
 SOFTWARE: PatentIN Ver. 2.1
 SEQ ID NO 7
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92.4%; Score 19.4; DB 4; Length 831;
Best Local Similarity 95.2%; Pred. No. 0.96;
Matches 20; Conservative 0; Mismatches 1; Indels
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92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94;
Matches 20; Conservative 0; Mismatches 1; Indels (
                               Query Match

92.4%; Score 19.4; DB 4; Length 694;
Best Local Similarity 95.2%; Pred. No. 0.94;
Matches 20; Conservative 0; Mismatches 1; Indels
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ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694 GCTTGGACTATAATACCTGAC 674
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                                                                                                                                                                       1 GCTTGGACTATAATACTTGAC 21
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ORGANISM: Brassica napus
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; LOCATION: (514)..(813)
US-09-794-384A-7
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US-09-733-151-39/c
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NAME/KEY: - . . 790
LOCATION: 9.. 790
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
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US-09-733-151-24/c
| Sequence 24, Application US/09733151
| Patent No. 6563026
| GENERAL INFORMATION:
| APPLICANT DE BOCH, et al.
| TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME; CURRENT PAPLICATION NUMBER: US/09/733,151
| CURRENT PAPLICATION NUMBER: 09/457,037
| PRIOR APPLICATION NUMBER: 09/457,037
| PRIOR FILING DATE: 1999-12-08
                                                                        DEFLICANT: DE BOCH, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATCHING DATE: 1999-12-08
SOFTWARE: PATCHIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
) LOCATION: (1)...(1077)
) OTHER INFORMATION: sequence comprising the 5' flanking region of RF-BN1
) NAME/KEY: misc_feature
) LOCATION: (1)...(45)
) OCTHER INFORMATION: pGEM-T vector
US-09-457-0378-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1). [(1077)]
COTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.4%; Score 19.4; DB 4; Length 1077; Best Local Similarity 95.2%; Pred. No. 0.99; Matches 20; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.4%; Score 19.4; DB 4; Length 1077; Best Local Similarity 95.2%; Pred. No. 0.99; Matches 20; Conservative 0; Mismatches 1; Indels 0.
Sequence 24, Application US/09457037B
Patent No. 6506963
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980 GCTTGGACTATAATACCTGAC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 1077
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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OTHER INFORMATION: /label= 3/g7
OTHER INFORMATION: /note= "3' regulatory sequence containing the OTHER INFORMATION: polyyadenylation site derived from Agrobacterium OTHER INFORMATION: T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "sequence derived from
tapetum specific promoter of Nicotiana tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= NPTII
/note= "coding sequence of neomycine
phosphotransferase gene"
                                                  NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
                                                                                                                                                                           COUNTRY: United States
ZIP: 22313-1404
ZOUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Parentin Release #1.0, Version #1.25
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,121
FLING DATE: 24-MAY-1993
CLASSIPELICATION DATA:
APPLICATION NUMBER: EP 9040332.1
FILING DATE: 23-MOV-1990
RRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 123-MOV-1990
RRIOR APPLICATION NUMBER: SP 91401888.2
FILING DATE: 08-JUL-1991
ATONNEY AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 36,113
TITLE OF INVENTION: PROCESS FOR TRANSFORMING TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1113 GCTTGGACTATAATACCTGAC 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1186 base pai
TYPE: nucleic acid
STRANDEDNESS: double
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NAME/KEY:
LOCATION: 791..1186
OTHER INFORMATION: /1.
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LOCATION: 1.8
OTHER INFORMATION: 
CTHER INFORMATION: 
FRATURE:
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Sequence 2, Application US/08064121 Patent No. 5641664 GENERAL INFORMATION: APPLICANT: D'HALLUIN, Kathleen

US-08-064-121-2

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/note= "sequence derived from tapetum specific promoter of Nicotiana tabacum"
                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                     PATENTE NO. BUGLOUN

GENERAL NIPORATION:
APPLICANT: GOBEL, Elke
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
TITLE OF INVENTION: MONOCOTYLEDONOUS PLANTS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathie STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria STREET: George Mason Bidg., Washington & Prince Sts.
CITY: Alexandria STREET: Pormitted States
CONTRY: United States
COMPUTE: Virginia
COMPUTE: ISP PC Compatible COMPUTE: ISP PC COMPABLIA
COMPUTE: ISP PC Compatible COMPUTE: ISP PC COMPABLIA
APPLICATION NUMBER: EP 91401888.2
FILING DATE: 04-JUL-1991
ATTORNEY/AGENT INFORMATION:
PELEPHONE: CANG-FEULY, Sharon
FELENOWINICATION NUMBER: 36.113
REFERENCE/DOCKET NUMBER: 36.113
REFERENCE/CHARACTERISTICS:
LENGTH 1186 base pairs
TTELEPHONE: COMPABLIA
TTELEPHONE: COMPABLIA
TTELEPHONE: COMPABLIA
TTELEPHONE: TTELE
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/note= "coding sequence of neomycine
phosphotransferase gene"
                            1; Indels
                        0; Mismatches
                                                                                                                                                          1113 GCTTGGACTATAATACCTGAC 1133
                                                                                    1 GCTTGGACTATAATACTTGAC 21
                                                                                                                                                                                                                                                            RESULT 15
US-08-475-975-2
; Sequence 2, Application US/08475975
; Patent No. 6002070
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MOLECULE TYPE: DNA (genomic)
HVDOTHRTICAL: NO
                               20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: probe FEATURE:
NAME/KEY:
LOCATION: 1..8
OTHER INPORMATION:
OTHER INFORMATION:
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LOCATION: 9..790
OTHER INFORMATION:
OTHER INFORMATION:
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                   Matches
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NAMPIKEY:
NAMPIKEY:
COATION: 791..1186
COTHER INFORMATION: /label= 3'g7
COTHER INFORMATION: /note= "3' regulatory sequence containing the polyadenylation
COTHER INFORMATION: site derived from Agrobacterium T-DNA gene 7"
US-08-478-015-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= NPTII
/note= "coding sequence of neomycine phosphotransferase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "sequence derived from
tapetum specific promoter of Nicotiana tabacum"
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RESULT 14
UG-08-478-015-2
UG-08-478-015-2
UG-08-478-015-5
Patent No. 5712135
Patent No. 5712135
Patent No. 5712135
Patent No. 5712135
PAPLICANT: GOBEL, Blke
PROCESS FOR TRANSFORMING
TITLE OF INVENTION: MONOCOTYLEDONGUS PLANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Burns, Doane, Swecker & Mathis STRET: P.O. Box 1404
CITY: Alexandria Acates
COUNTY: Alexandria COUNTY: United States
ZIP: 22311-1404
CITY: MisspalalE FORM:
MEDIUM TYPE: FLOPPY disk
CONNTYER: TEM PC compatible.
CONNTYER: PRADABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
CONNTYER: PRADABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: DEADTH NOWER: OF-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: PC-DOS/MS-DOS
CONNTYER: DAPLICATION DATA:
APPLICATION NUMBER: BP 91401888.2
FILING DATE: 23-NOV-1990
PRIOR APPLICATION NUMBER: US 08/064,121
PRIOR APPLICATION NUMBER: US 
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.4%;
95.2%;
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LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
NAME/KEY:
LOCATION:
CTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: probe
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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us-09-698-903b-12.rni

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ó;
) OTHER INFORMATION: /label= 3/g7 OTHER INFORMATION: /note= "3' regulatory sequence containing the COTHER INFORMATION: polyadenylation site derived from Agrobacterium US-08-475-975-2
                                                                                                                            Query Match 92.4%; Score 19.4; DB 3; Length 1186;
Best Local Similarity 95.2%; Pred. No. 1;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: December 5, 2004, 07:17:54 Job time : 4.528 secs

Sequence 3, Appli Sequence 3, Appli Sequence 144465, Sequence 144465, Sequence 144465, Sequence 28593, A Sequence 2101, Appli Sequence 2101, Appli Sequence 352, Appli Sequence 261250, Sequence 261251, Sequence 261251,

1728 1728 90541 90541 90541 9668 844 844 850 1677 2016 2016 2017 41156 44495 94495 94495 94495

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NAME/KEY: unsure
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Sequence 5059, Ap
Sequence 239504,
Sequence 239505,
Sequence 239505,
Sequence 2, Appli
Sequence 11151, A
Sequence 143567,
Sequence 97619, A
                                                                                                                                             2004, 06:58:29 ; Search time 18.2949 Seconds (without alignments) 6907.991 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

| cgn2_6/ptodate12/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodate12/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/DG6_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodate12/pubpna/US06_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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0.05-09-923-876-5059

3.05-10-027-632-239504

5.05-10-027-632-239504

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3.05-10-027-632-143567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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23
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572
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478
628
628
628
1728
                                                                                                                                                  2,
                                                                                                                                                    December
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80.0
80.0
80.0
80.0
73.7
75.7
                                                                                                                                                                                                                                  Title:
Perfect score:
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                                                                                                          OM nucleic
                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                    Run on:
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No.
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Sequence 3470, Ap

US-09-764-877-3470

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RESULT.

US-09-923-876-5059/c

Sequence 5059, Application US/09923876

Patent No. US2002001358A1

Sequence 5059, Application US/09923876

Patent No. US2002001358A1

APPLICANT: Radigaki, Leara Y. (Ico)

APPLICANT : Radigaki, Leara Y. (Ico)

FRIOR RILNG DATE: 1998-06-06

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 6332

SOFTWARE: PROGRAM: Instruction No. US20020013958A1 700456286H1

NAME/KRY: misc feature

SEQ ID NOS: 6326

CONCATION: SOFTWARTION: Locyte ID No. US20020013958A1 700456286H1

NAME/KRY: unsure

COCATION: SOFTWARTION: A. t. c. g, or other

US-09-23-876-5059

QUERY MARCH

Best Local Similarity 87.0%; Pred No. 63;

Best Local Similarity 87.0%; Pred No. 6
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Query Match
Best Local Similarity 95.03
Matches 19; Conservative
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        ) ORGANISM: Human
US-10-027-632-239504
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                                                                                                                                                                                                             Sequence 5059, Application US/09923876

Publication No. US20030237110A9

GENERAL INCORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ealgudi, Bradnath V.
APPLICANT: ASserman, Bradley K.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: 2-0012-1 CON
CURRENT APPLICATION NUMBER: 05/09/923,876

CURRENT APPLICATION NUMBER: 09/298,329

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR PLILNG DATE: 1999-04-21

PRIOR PLILNG DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram

SEQ ID NO 5059

LENGTH: 173
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/27,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1099-11-23

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/166,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-28

PRIOR FILI
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OTHER INFORMATION: Incyte ID No. US20030237110A9 700456286H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
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87.0%; Pred. No. 63
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LOCATION: 58, 115, 143

OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-5059
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Publication No. US20020198371A1
GENERAL INFORMATION:
129 GACATCCATGTAACNCAGCAGGG 107
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Best Local Similarity 87.04
Matches 20; Conservative
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US-09-923-876-5059/c
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Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Dolymorphisms in the Human Genome

FILE OF INVENTION: POLYMORPHISMS in the Human Genome

FILE OF INVENTION: 108037.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1909-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-03-28

PRIOR FILING DATE: 1999-03-38

PRIOR PLING DATE: 1999-03-38

PRIOR FILING DATE: 1999-03-38

PRIOR PLING DATE: 1999-03-38

PRIOR FILING DATE: 1999-03-38

PRIOR PLING DATE: 1999-03-38
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 10882 7.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
                                                                                     Gaps
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        Length 572;
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Score 18.4; DB 13;
Pred. No. 1.2e+02;
0; Mismatches 1;
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95.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 1;
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Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                                                                                          369 AAAGCCATGTAAAGCAGCAG 350
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Query Match
Best Local Similarity 95.0%;
Matches 19; Conservative
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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95.0%; Pred. No. 2e+02;
tive 0; Mismatches
                                 PRIOR APPLICATION UNMBER: 2002-11-13
PRIOR APPLICATION NUMBER: PCT/EPO2/01867
PRIOR FILING DATE: 2002-02-21/PC02/01867
PRIOR PELING DATE: 2002-02-21/PC044.7
PRIOR PELING DATE: 2001-07-02
PRIOR PELING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 58
SOCIETA PACENTIN NOS: 58
SOCIETA NOS: 58
LENGTH: 16570
LENGTH: 16570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELING DATE: 2001-05-23
PRIOR PELING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-36
PRIOR PELING DATE: 2000-06-36
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR PELING DATE: 2000-09-37
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
FILE REFERENCE: 2923-212
CURRENT APPLICATION NUMBER: US/10/275,287
CURRENT FILING DATE: 2002-11-13
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APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11151, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12888 GAAGTCCATGTAAAGCAGCA 12869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAATCCATGTAAAGCAGCA 20
                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human cytomegalovirus
US-10-275-287-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.0
Matches 19; Conservative
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US-09-864-761-11151/c
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Publication No. US20040087001A1
GENERAL INFORMATION:
TITLE OF INVENTION: Recombinant vector containing infectious human cytomegalovirus ge
TITLE OF INVENTION: with preserved wild-type characteristics of clinical isolates
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PAPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-09-38
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRAESEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.0%; Score 18.4; DB 15; Length 572; Best Local Similarity 95.0%; Pred. No. 1.2e+02; Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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Pred. No. 1.2e+02;
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      PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: F8stSEQ for Windows Version 4.0
SEQ ID NO 239504
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Publication No. US20030204075A9
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Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-239504
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US-10-027-632-239505
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Sequence 143667; Application US/10027632

Sequence 143667; Application US/10027632

SEDERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108877.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR APPLICATION NUMBER: US 60/128,006

PRIOR PILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/165,358

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FRASERE FEASERE FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.1%; Score 18.2; DB 9; Length 478; Best Local Similarity 87.0%; Pred. No. 1.4e+02; Matches 20; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                             FEATURE:

OTHER INFORMATION: MAP TO ACOOSO83.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.48

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.78

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.43

OTHER INFORMATION: EXPRESSED IN BOUR MARROW, SIGNAL = 0.6

US-09-864-761-11151
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION WUMBER: US 09/774,203
WINDR FLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11151
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 GACATCCATGTAAGGAAGCAGGG 294
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                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Matches 18; Conserv
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US-10-027-632-143567
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; Sequence 143567, Application US/10027632; Publication No. US20030204075A9

RESULT 10 US-10-027-632-143567

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WERTICANTY (ARM THOUSE)

WINDERENCY (ARM THOUSE)

FILE OF INVERTION: Delymorphisms in the Human Genome
FILE REPERRORS. 10807.129

CURRENT APPLICATION NUMBER: US 60/198,006

PRICOR PRILICATION NUMBER: US 60/198,006

PRICOR PRILICATION NUMBER: US 60/198,006

PRICOR FILIND DATE: 2000-2-24

PRICOR FILIND DATE: 2000-2-2-3

PRICOR FILIND DATE: 2000-2-2-3

PRICOR FILIND DATE: 2000-2-2-3

PRICOR FILIND DATE: 2000-2-3-3

PRICOR FILIND DATE
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Length 1728;

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Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/09759359A
Sequence 3, Application US/0804360A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT APPLICATION NUMBER: 2001-01-16
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-1U-1Z/-624-9/14/5/C
Sequence 97619, Application US/10027632
Publication No. US2003020407549
Publication No. US2003020407549
Publication No. US2003020407549
FURBEAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Human Genome
FILE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Identification NUMBER: US 60/128, 006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-103-28
PRIOR FILING DATE: 1999-103-38
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                                                                                                                                                                                                                                                                                                                                                                             75.7%; Score 17.4; DB 15; 94.7%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 97618
LENGTH: 1728
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Best Local Similarity 94.7
Matches 18; Conservative
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US-10-027-632-97619
                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-97618
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US-09-759-359A-3
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sequence 97619, Application US/10027632
publication No. US20020193371A1
publication No. US20020193371A1
publication No. US20020193371A1
publication No. US2002019371A1
publication No. US2002019371A1
publication No. US2002014
publication Sequence Sequen
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Sequence 97618, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR PLILNG DATE: 2000-07-12

PRIOR PLILNG DATE: 2000-07-12

PRIOR PLILNG DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PLILNG DATE: 10000-03-24

PRIOR PLILNG DATE: 1000-03-24

PRIOR PLILNG DATE: 1000-03-24

PRIOR PLILNG DATE: 1090-03-24

PRIOR PLILNG DATE: 1090-03-28

PRIOR PLILNG DATE: 1090-03-28

PRIOR PLILNG DATE: 1099-09-28

PRIOR FILING DATE: 1099-09-28

PRIOR FILING DATE: 1099-09-28
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                      1; Indels
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Pred. No. 4.2e+02;
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75.7%; Score 17.4; D
Best Local Similarity 94.7%; Pred. No. 4.2e
Matches 18; Conservative 0; Mismatches
                      0; Mismatches
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                                                                                                                                                                                  1710 GAATCCATGTAAAGCACC 1692
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                      18; Conservative
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US-10-027-632-97618/c
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US-10-027-632-97619
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                          Matches
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Indels

Length 1728;

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; SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DA
; ORGANISM: Human
US-09-759-359A-3

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 9; Length 90541;
Best Local Similarity 94.7%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps

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AATCCATGTAAAGCAGCAG

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Saarch completed: December 5, 2004, 09:36:24
Job time: 20.2949 secs
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us-09-698-903b-11.rni

Page 1

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RESULT 1
US-09-430-497A-11
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                                                                                              December 5, 2004, 05:20:20 ; Search time 3.864 Seconds (without alignments) 4230.886 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                        lssued_Patents NA:*
1: /cgn2 6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/1/ina/AB_COMB.seq:*
5: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
6: /cgn2 6/ptodata/1/ina/PCTUS COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 824507 seqs, 355394441 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                1 gaaatccatgtaaagcagcaggg 23
                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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23
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                      Searched:
                                                                                                 Run on:
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No.
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RESULT 2
US-09-430-497A-8

Sequence 8, Application US/09430497A

Sequence 8 Application US/09430497A

Sequence 8 Application US/09430497A

Sequence 8 Application US/09430497A

Sequence 8 Application US/09430497A

TEREPERENTINON: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING CURRENT FULING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 8

LENGTH: 415

TYPE: DA

ORGANISM: Artificial Sequence

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Patent No. 650916
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-TERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: AME
FILE REPERENCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 199-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 23
                                                           260, App
25, App
25, App
25, App
25, Ap
25, Ap
27, App
28, App
28, App
28, App
29, App
21, App
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OTHER INFORMATION: Description of Artificial Sequence: primer MDB371 US-09-430-497A-11
     Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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US-09-372-498-9
US-09-513-999C-260
US-08-708-708-25
US-08-708-708-25
US-09-238-471-25
US-09-288-708-5985
US-09-688-097A-1
US-09-688-097A-1
US-09-688-097A-1
US-08-899-371-2
US-08-899-371-1
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US-09-68-183
US-09-713-550-183
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US-09-64-173-185
US-09-64-173-185
US-09-64-173-185
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100.0%; Score 23; DB 4;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 23; Conservative 0; Mismatches 0;
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Gaps

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Length 90541;

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICAMY: ABD'THREIDEH, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOO1043

CURRENT PILITIO DATE: 2002-07-31

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.7%; Score 17.4; DB 4; Length 90541; 94.7%; Pred. No. 1.2e+02; 1.ve 0; Mismatches 1; Indels 0;
                                                                                       Score 17.4; DB 4;
Pred. No. 1.2e+02;
                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) Sequence 352, Application US/09620312D ; Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AAATTCATCTCAAGCAGCAGGG 272
                                                                                                                                                                                                                  66140 AATCCATGTAAAGGAGCAG 66158
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                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10207973
Patent No. 6753175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13425
                                                                                                                                                                            3 AATCCATGTAAAGCAGCAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,0
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                                                                                       Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Conservative
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-270-767-13425/c
                              , ORGANISM: Human
US-09-759-359A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-620-312D-352
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                                                                                                                                                                                                                                                                               RESULT 5
US-10-207-973-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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APPLICANT: ABU-THREIDEH, Jane et al
TITLE OF INVENTION:
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1043
CURRENT FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 3: LENGTH: 90541
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US-09430-497A-10/c
Sequence 10, Application US/09430497A
Factor 10. 6509516
GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELER, Marc
TITLE OF INVENTION: SAME
FILE REFERENCE: 514412-029
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                             Gaps
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OTHER INFORMATION: Description of Artificial Sequence: 3' border OTHER INFORMATION: flanking region of elite event MS-B2
NAME/KSY: misc feature
LOCATION: (1). (193)
OTHER INFORMATION: T-DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; DB 4; Length 416; 100.0%; Pred. No. 0.077; tive 0; Mismatches 0; Indels
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: flanking region of elite event MS-B2 NAME/KEY: misc_feature LOCATION: (1). (234)
                                                                                                                                                                                                                                                                                                                                 152 GAAATCCATGTAAAGCAGCAGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 GAAATCCATGTAAAGCAGCAGGG 241
                                                                                                                                                                                                                                                                                                1 GAAATCCATGTAAAGCAGCAGGG 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                   OTHER INFORMATION: plant DNA NAME/KEY: misc feature LOCATION: (235). (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (194)...(416)
OTHER INFORMATION: plant DNA
                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
"...hes 23; Conservative
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Best Local Similarity 100.0
Matches 23, Conservative
                                                                                                                          ) OTHER INFORMATION: T-DNA
US-09-430-497A-8
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Gaps

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Sequence 13425, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13425
LENGTH: 1909
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 65;
0; Mismatches
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APPLICATION NUMBER: US/08/894,344C
FILING DATE: 15-AUGUST-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP343700/95
FILING DATE: 28-DECEMBER-1995
APPLICATION NUMBER: PCT/JP96/03862
FILING DATE: 27-DECEMBER-1996
ATTORNEY/AGENT INFORMATION:
NAME: PERTY LAWFENCE S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212-218-2100
TELEFAX: 212-218-2200
INFORMATION FOR SEQ ID NO: 1 :
SEQUENCE CHARACTERISTICS:
LENGTH: 8874 base pairs
TYPE: nucleic acid
STRANDEDISS: double
TOPOLOGY: linear
MOLECTLE TYPE: Genomic DNA
ORGANISM: SACCHAROMYCES CETEVISIAE
STRANDEN: 220-1B
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APPLICANT: KAMASAKI, Hideki
APPLICANT: TOKAI, MASAYA
APPLICANT: TOKAI, MASAYA
APPLICANT: KIKUCHI, Yasuhiro
APPLICANT: WINCHI, KOZO
TITLE OF INVENTION: DOW TENSOR
TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
NUMBER OF SEQUENCES:
ADDRESSE: FITZPATRICK, CELLA, HARPER & SCINTO
STREET: 30 ROCKEFELIER Plaza
CUTY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETE - 3.50 inch, 1440 Kb storage.
COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AND VET.0
CURRENT APPLICATION DATA:
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74.8%; Score 17.2; DB 4; Length 4495;
Best Local Similarity 86.4%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drmanac, Radoje T.
TITLE OP INVENTION: No. 6569662e1 Nucleic Acids and
TITLE OP INVENTION: Polypeptides
TITLE OP INVENTION: Polypeptides
FILE REPERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312B
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFUMARS: PL_Genes Version 1.0
SEQ ID NO 352_
LENGTH: 4495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3034 AACTCCTTGTAAAGCAGCAGAG 3055
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GENERAL INFORMATION:
                                                                   Liu, Chenghua Asundi, Vinod Zhang, Jie Ren, Feiyan Chen, Rui-hong Zhao, Qing A. Wehrman, Tom Xue, Aidong J. Yang, Yonghong Wang, Jian-Rui Zhou, Ping Ma, Yunqing Wang, Dunrui Wang, Zhiwei John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (307)..(3006)
US-09-620-312D-352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-894-344C-1/c
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FEATURE:
NAME/KEY: CDS

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US-09-125-028-1/C
US-09-125-028-1/C
Sequence 1, Application US/09125028A
Sequence 1, Naplication US/09125028A
Sequence 1, NeoMartion:
Patent No. 6190707
GENERAL INFORMATION:
APPLICANT: COLAVIZZA, Didier
APPLICANT: COLAVIZZA, Didier
TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
TITLE OF INVENTION: NOWER: US/09/125,028A
CURRENT APPLICATION NUMBER: US/09/125,028A
CURRENT APPLICATION NUMBER: US/09/125,028A
GERLIER FILING DATE: 1997-02-07
HARMARE: PATENTION TOWE: 2.1
SEQ ID NO 1
LENGTH: 9621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7552 AAATTAATGTAAAGCACCAGGG 7531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                LOCATION: 4388 to 4393 IDENTIFICATION METHOD: S
                                                                                                                                                                                                                                             NAME/KEY: cleavage-site
LOCATION: 5927 to 5032
IDENTIFICATION METHOD: 9
                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: cleavage-site
LOCATION: 7675 to 7680
IDENTIFICATION METHOD:
                                                                                                                                 FEATURE:
NAME/KEY: cleavage-site
                                          FEATURE:
NAME/KEY: cleavage-site
LOCATION: 1291 to 1296
IDENTIFICATION METHOD:
LOCATION: 1 to 8874 IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: 0639063
; Sequence 15579, Application US/09621976
; Patent No. 6639063
; Patent No. 6639063
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Obbert, S.
; APPLICANT: Obbert, S.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15579
; LENGTH: 446
    TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1416
LENGTH: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
FILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SSOFWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                  FEATURE:

NAME/KEY: CDS

LOCATION: 67..130

NAME/KEY: 819_Deptide

LOCATION: 67..126

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 8.33999961853027

CTHER INFORMATION: seq AVVGCLLVPPAEA/NK

US-09-621-976-1416
                                                                                                                                                                                                                                                                                                                                                                                                                                     72.2%; Score 16.6; D
82.6%; Pred. No. 89;
tive 0; Mismatches
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Pred. No. 91;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 GAAGGCCATGTAGAGCAACAGGG 367
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Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.6%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.55
Best Local 19; Conservative
                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15579
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US-09-621-976-181/c
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                                                                                                                                                       Length 9621;
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                                                                                 ; OTHER INFORMATION: Use of n signifies any of g, a, c or t US-09-125-028-1
                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTICIA:
LOCATION: (47)
OTHER INFORMATION: a, c, g, t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: a, c, g, t, unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;; LOCATION: (273)
;; OTHER INFORMATION: a, c, g, t, unknown or other 15-09-655B-3
                                                                                                                                                                                                                                                                                                                                   RESULT 10

US-09-720-655B-3/C

Sequence 3, Application US/09720655B
Patent No. 6723521
GENERAL INFORMATION;
APPLICANT: YOSHIMOTO, MAKOTO
APPLICANT: YOSHIMOTO, KAYO
APPLICANT: MATSUMOTO, KAYO
APPLICANT: TAKAYAMA, KIYOSHI
ITILE OF INVENTION: SUGAR TRANSPORTER
FILE REFERENCE: ASA-C034
CURRENT FILING DATE: 1090-02-28
FRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 8
                                                                                                                                              Query Match
74.8%; Score 17.2; D
Best Local Similarity 86.4%; Pred. No. 94;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.2%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                         7927 AAATTAATGTAAAGCACCAGGG 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 GAAGTGAATGCAAAGCAGCAGGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-621-976-1416/c
Sequence 1416, Application US/09621976
Petent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: diordano, J.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                    2 AAATCCATGTAAAGCAGCAGGG 23
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (36)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified_base LOCATION: (251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified base
LOCATION: (273)
                    FEATURE:
NAME/KEY: misc feature
LOCATION: (9318)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3
LENGIH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Query Match
72.2%; Score 16.6; DB 4; Length 1571;
Best Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0;
                                              Query Match
Pest Local Similarity 82.6%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: December 5, 2004, 07:17:53 Job time : 4.864 secs
                                                                                                                                                                                                                                                                                 836 GAAATCCAGGAAAAGCAGAAGAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 GAAGGCCATGTAGAGCAACAGGG 411
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                                                                                                                                                                                                        1 GAAATCCATGTAAAGCAGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-673-395A-3/c
; Sequence 3, Application US/09673395A
; Patent No. 6620923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
US-09-107-532A-2051
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Sequence 2051, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BNIEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLOWASITY AS IN COMMERCE AND SERVICE AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
72.2%; Score 16.6; Dest Local Similarity 82.6%; Pred. No. 95; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1416
SEQUENCE DESCRIPTION: SEQ ID NO: 2051:
                                                                                                                                                  NAME/KEY: CDS
10CATION: 309.542
NAME/KEY: sig_peptide
10CATION: 309.455
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.0999990463257
COTHER INFORMATION: seq_LLXMAFLMLGGFS/DP
US-09-621-976-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 gaaggccargrangagcaacaggg 412
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-107-532A-2051
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               LENGTH: 542
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Gaps

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Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

December 5, 2004, 06:58:29; Search time 330.898 Seconds (without alignments) 6907.991 Million cell updates/sec Run on:

US-09-698-903B-10 416

1 ctacggcaatgtaccagctg............atgaacacccaaactcgat 416 Title: Perfect score: Sequence:

IDENTITY NUC Gapoxt 1.0 Scoring table:

3694831 segs, 2747406616 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/USO7_pUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 5, Appli	Sequence 5, Appli	Seguence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Seguence 24, Appl	Sequence 24, Appl	Sequence 13, Appl	Sequence 100, App
ΩI	US-10-027-880-5	9 US-09-509~945-5	US-09-509-945-4	US-09-733-151-2	US-10-375-332-2	US-09-733-151-1	US-10-375-332-1	US-09-970-921-7	US-09-733-151-24	US-10-375-332-24	US-10-047-542-13	US-10-047-542-100
DB	15	σ	σ	σ	15	σ	15	σ	o,	15	13	13
Query Match Length DB	7599	6539	6548	4832	4832	4946	4946	5349	1077	1077	4465	6602
Query Match	46.3	45.7	45.7	45.6	45.6	45.6	45.6	45.6	43.0	43.0	37.2	37.2
Score	192.6	190	190	189.6	189.6	189.6	189.6	189.6	179	179	154.6	154.6
Result No.	, 1 1 1 1 1	7	m	Ω	Ŋ	ω υ	0	ω	o U	, c 10	11	12

0 0 4 4 0	Sequence Seq	Sequence 4, Appli Sequence 5, Appli Sequence 4, Appli Sequence 23, Appl		equence quence equence equence equence	Sequence 9, Appl.1 Sequence 39, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 179, Appl
US-10-047-542-1 US-10-047-542-1 US-09-847-057-4 US-09-874-926-4 US-10-250-821-2	US-10-250-55 US-10-250-82 US-10-250-55 US-10-250-82 US-10-250-55	US-10-948-13 US-10-033-1 US-10-407-8 US-10-250-8	US-10-250-821-2 US-10-250-821-2 US-10-250-821-2 US-10-250-821-2 US-10-250-83-2 US-10-250-83-2	US-10-033-190- US-09-794-384A- US-10-801-552- US-09-940-550A US-09-792-568-	ם ם
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7129 8074 8340 8340 12079	12079 12085 12085 12093 12093	12241 12241 12241 13002	13905 13905 13905 15430 17752 17752	10078 831 831 7129 9901	12438 694 694 909 909 163382
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ALIGNMENTS

Sequence 5, Application US/10027880

Sequence 5, Application US/10027880

Publication No. US20030106105A1

GENERAL INFORMATION:
TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY IN PLANT ROOT CELLS,
TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED

TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED

FILE REFERENCE: CHEP:003US

CURRENT APPLICATION NUMBER: US/10/027,880

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: POT/FR00/01768

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 5

LENGTH: 7599 TYPE: DNA ORGANISM: Artificial Sequence PEATURE: CHER INFORMATION: Description of Artificial Sequence: T-DNA of pGKBS US-10-027-880-5

ö 09 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 0; Gaps Query Match
Best Local Similarity 99.5%; Pred. No. 1.1e-29;
Matches 192; Conservative 1; Mismatches 0; Indels 0;

6579 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTCTGAATTTAAACTTGC 6638 ΒÞ ò

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Sequence 2, Application US/09733151
Patent No. US20010029620A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERBENCE:
514412-2019
CURRENT FILING DATE: 2000-12-08
FRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR PELING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10375332
Publication No. US20030188347A1
Publication No. US20030188347A1
APPLICANT: De Both, et al.
ITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
                                                                                                                                                                                                                                                                                                 6471 TAITTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
                                                                                                                                                                                                                             6411 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 6470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
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                                                                                              1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                    6351 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTTAAACTTGC
                                                                                                                                                                                   61 ATCAATAAAWITAIGITITIGCITGGACTATAATACCIGACTIGITATTITATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4832;
Score 190; DB 9; Length 6548; Pred. No. 3.6e-29; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.6%; Score 189.6; DB 9; Best Local Similarity 99.5%; Pred. No. 3.9e-29; Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COCATION: (1)...(4832)
CTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
  Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           5531 GACCATGTACGT 6542
                                                                                                                                                                                                                                                                                                                                                            181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GACCATGTAC 190
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NAME/KEY: misc_feature
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US-10-375-332-2/c
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                                                                                                                                                                                                                                                       Sequence 5. Application US/09509945
Patent No. US20020166140A1
GENERAL INFORMATION:
APPLICANT: HAWADA, KAZUYUKi et al.
TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
TITLE OF INVENTION NUMBER: US/09/509,945
CURRENT APPLICATION NUMBER: US/09/509,945
CURRENT APPLICATION NUMBER: US/09/509,945
SUBJECT OF SEQ ID NOS: 7
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
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Pactent No. US2002016640A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MATANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REFERENCE: 0230-0148P

CURRENT FILING DATE: US/09/509,945

CURRENT FILING DATE: 201-04-01

NUMBER OF SEQ ID NOS: 7

SOOTHARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 6448
                                                               6699 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6758
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OTHER INFORMATION: Clone: pTS431
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ORGANISM: Escherichia coli LE392
PEATURE:
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; OTHER INFORMATION: Clone: pTS172
US-09-509-945-4
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US-09-509-945-5
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US-09-509-945-4
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us-09-698-903b-10.rnpb

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183 ATCAATAAATTTATGTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEX: misc_feature
; LOCATION: (1)...(4946)
; OTHER INFORMATION: Plasmid pTHW107
US-10-375-332-1
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-970-921-7/c
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LENGTH: 5349
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Sequence 1, Application US/09733151

Sequence 1, Application US/09733151

Sequence 1, Application US/09733151

GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE EFFERENCE: 500-12-08

CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SEQ ID NO: 1

LENGTH: 4946
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45.6%; Score 189.6; DB 9; Length 4946;
Best Local Similarity 99.5%; Pred. No. 4e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
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45.6%; Score 189.6; DB 1.
Best Local Similarity 99.5%; Pred. No. 3.9e-29;
Matches 189; Conservative 1; Mismatches 0
         FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
PURRENT FILING DATE: 2003-02-27
PURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PERCENTIN VERSION 3.0
SEQ ID NOS: 43
LENGTH: 4832
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NAME/KEY: misc feature

LOCATION: (1). (4946)

OTHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature; DCATION: (1)..(4832)
OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2
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RESULT 7

US-10-375-332-1/c

US-10-375-332-1/c

i gaquence 1, Application US/10375332

publication No. US20030188347A1

i GENERAL INFORMATION:

APPLICANT: De Both, et al.

TILE OF INVENTION: HYBRED WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME

FILE REPRENCE: 514412-2019

CURRENT APPLICATION NUMBER: US/10/375,332

CURRENT FILING DATE: 2003-02-27

PRIOR FILING DATE: 2003-02-27

PRIOR PRICK APPLICATION NUMBER: 09/457,037

PRIOR PLING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 4946 ö 120 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180 243 CTACGGCAAIGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 184 124 121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTTCTTATC 180 09 64 61 ATCAATAAAWTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 123 TATTTAAACTATATTICTTICAAGATGGGAATTAACATCACAAATTGCCTTTTCTTATC 1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 0; Gaps Query Match
Best Local Similarity 99.5%; Pred. No. 4e-29;
Matches 189; Conservative 1; Mismatches 0; Indels 0;

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APPLICANT: De Both, et al.
TILE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 1077
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| NAME/KEY: misc_feature
| LOCATION: (3370)...(4245)
| OTHER INPOMATION: label = synb*; "improved barstar DNA"
| NAME/KEY: misc_feature
| LOCATION: (4346)...(4577)
| OTHER INPOMATION: label = 3'chs, "region containing 3' untranslated
| OTHER INPOMATION: end of chalcone synthase gene"
| NAME/KEY: misc_feature
| LOCATION: Complement((5225)...(5349))
| OTHER INPOMATION: label = LB, "T-DNA left border"
| US-09-970-921-7
                                                                                OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                             NAME/KEY: misc feature
LOCATION: Complement((1)..(25))
CTHER INFORMATION: label = RB, "T-DNA right border"
NAME/KEY: misc feature
LOCATION: Complement((98)..(331))
OTHER INFORMATION: label = 3'97, "region containing 3' untranslated
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
NAME/KEY: misc feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin
OTHER INFORMATION: acetyl transferase"
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LOCATION: Complement (1884)...(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Virus"
NAME/KEY: misc feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO OTHER INFORMATION: 92/13956)"
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Pred. No. 4.1e-29;
1; Mismatches 0; Indels
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; Patent No. US20010029620A1
; GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 99.5%;
Matches 189; Conservative
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US-09-733-151-24/c
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GENERAL INVOCATION.

GENERAL INVOCATION.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE SPERRENCE: 5144412-2019

CURRENT APPLICATION NUMBER: US/10/375,332

CURRENT FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: 09/457,037

PRIOR FILING DATE: 1009-112-08

PRIOR FILING DATE: 09/457,037

PRIOR PLING DATE: 09/457,037

PRIOR FILING DATE: 1999-112-08

SOFTWARE: Patentin version 3.0

SEQ ID NO 24

LIENGTH: 1077
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; TYPE: DNA
) GRGANISM: Brassica napus
) FRATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)..(1077)
| CTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
18-09-733-151-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1). (1007)
OTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1
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Pred. No. 3.7e-27;
1; Mismatches 1;
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                                                                                                                                                                   Query Match
Best Local Similarity 98.9%;
Matches 179; Conservative
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Best Local Similarity 98.9%;
Matches 179; Conservative
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US-10-375-332-24/c
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US-10-047-542-14/c
; Sequence 14, Application US/10047542
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Publication No. US20020168367A1;
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: NOVEL INMUNOADHESINS FOR TREATING AND PREVENTING VIRAL;
TITLE OF INVENTION: AND BACTERIAL DISEASES
FILE REFRENCE: 030905.0004.01P1
CURRENT PAPLICATION NUMBER: PCT/US01/13932
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR FILING DATE: 2001-04-28
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PATCHILL OF THE PATCHILL OF THE
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| LOCATION: (2214)...[2215)

| CHER INFORMATION: a, c, t or

US-10-047-542-13
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.4*
Matches 154; Conservative
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US-10-047-542-100
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US-10-047-542-13
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Sequence 101, Application US/10047542

| Sequence 101, Application No. US202020168367A1
| Publication No. US202020168367A1
| General IRPORMATION:
| APPLICANT LARRICK, JAMES W. |
| APPLICANT: WYOOFF, KEITH L. |
| TITLE OF INVENTION: NOVEL IMMUNABHESINS FOR TREATING AND PREVENTING VIRAL |
| TITLE OF INVENTION: AND BACTERIAL DISEASES |
| FILE REFERENCE: 03095.0004.CIP1 |
| CURRENT PILING DATE: 2001-04-26 |
| FRIOR FILING DATE: 2001-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| NUMBER OF SEQ ID NOS: 101 |
| SEQ ID NO 101 |
| LENGTH 1139
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                                                                                                                                                                                                                                   Length 6602;
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                                                                                                                                                                                                                           Query Match
37.2%; Score 154.6; DB 13; Length
Best Local Similarity 99.4%; Pred. No. 6.7e-22;
Matches 154; Conservative 1; Mismatches 0; Indels
; SEQ ID NO 100

LENGTH: 6602

TENGTH: 6602

ORGANISM: ORGANISM: TENGTNES:

PEATURE:

OTHER INFORMATION: Description of Unknown Organism:

OTHER INFORMATION: pGPTV-kan-ocs-ATR-IgA2
US-10-047-542-100
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US-10-047-542-101/c
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6588 ATCAATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAA 6529
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Job time : 331.898 secs
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TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
FILE REPERENCE: PAGODA
CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                            JAPELICANT: LARRICK, JAMES W.
APPLICANT: MYCOPF, KEITH L.
JITLE OF INVENTION: NOTE LEMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
TITLE OF INVENTION: AND BACTERAL DISEASES
FILE REFERENCE: 030905.0004.CIPI
CURRENT APPLICATION NUMBER: US/10/047.542
CURRENT FILING DATE: 2000.04-28
PRIOR APPLICATION NUMBER: PCT/US01/13932
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
SPRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
PRIOR PILING DATE: 2000.04-28
SOFTWARE: BALCATION NUMBER: 60/200,298
PRIOR PILING DATE: 2000.04-28
SOFTWARE: PALCATION NUMBER: 60/200,298
PRIOR PILING DATE: 2000.04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  887 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.2%; Score 154.6; DB 13; Length 8074; Best Local Similarity 99.4%; Pred. No. 7.2e-22; Matches 154; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.2%; Score 154.6; DB 9; Length 8340; Best Local Similarity 99.4%; Pred. No. 7.2e-22; Matches 154; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Expression-type plasmid pBMSP-1spJSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                767 TATTTAACTATATTCTTTCAAGATGGGAATTAA 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09847057
Patent No. US20020004943Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
; ORGANISM: Binary vector pAGI4002
US-09-847-057-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: modified_base
LOCATION: (2315)
OTHER INFORMATION: a, c, t or g
Publication No. US20020168367A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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OM nucleic - nucleic search, using sw model

December 5, 2004, 05:20:20 ; Search time 69.888 Seconds (without alignments) 4230.886 Million cell updates/sec Run on:

US-09-698-903B-10 416

Title: Perfect score: Sequence:

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824507 segs, 355394441 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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189.6 45.6 1303 3 US-09-458-093-2 Sequence 2, 189.6 45.6 3200 1 US-08-694-824-23 Sequence 2, 189.6 45.6 3200 1 US-08-694-824-23 Sequence 2, 189.6 45.6 4832 4 US-09-457-0378-23 Sequence 2, 189.6 45.6 4846 4 US-09-457-0378-1 Sequence 2, 189.6 45.6 4946 4 US-09-457-0378-1 Sequence 1, 189.6 45.6 4946 4 US-09-457-0378-1 Sequence 1, 189.6 45.6 5349 4 US-09-757-0178-1 Sequence 1, 189.6 45.6 5349 4 US-09-970-921-7 Sequence 1, 189.6 45.6 5560 3 US-09-70-91-7 Sequence 2, 189.6 45.6 5560 3 US-09-430-497A-1 Sequence 2, 189.6 45.6 5562 4 US-09-430-497A-1 Sequence 2, 189.6 45.6 5563 3 US-08-232-016-23 Sequence 2, 189.6 45.6 7639 2 US-08-232-016-23 Sequence 2, 189.6 45.6 7639 2 US-08-894-440-4 Sequence 2, 189.6 45.6 7639 2 US-08-894-440-4 Sequence 2, 189.6 45.6 7639 2 US-08-894-440-4 Sequence 2, 179 43.0 1077 4 US-09-457-0378-24 Sequence 24,	0		45.6	1303	m	08-894-440-	7
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189.6 45.6 4832 4 US-09-457-037B-2 Sequence 2, 189.6 45.6 4848 4 US-09-733-151-2 Sequence 2, 189.6 45.6 4946 3 US-09-817-188-1 Sequence 1, 189.6 45.6 4946 4 US-09-457-037B-1 Sequence 1, 189.6 45.6 5349 3 US-09-733-151-1 Sequence 1, 189.6 45.6 5349 4 US-09-70-21-7 Sequence 1, 189.6 45.6 5540 3 US-09-970-91-7 Sequence 7, 189.6 45.6 5560 3 US-09-970-91-7 Sequence 2, 189.6 45.6 562 US-09-232-016-23 Sequence 2, 189.6 45.6 7539 2 US-08-232-016-23 Sequence 2, 188.45.2 5864 3 US-09-440-4 Sequence 2, 188.45.2 5864 3 US-09-45-037B-24 Sequence 24, 179 43.0 1077 4 US-09-457-037B-24 Sequence 24,	_	189.6	45.6	3200	71	08-694-824	23,
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189.6 45.6 7566 2 US-08-232-016-23 Sequence 23, 189.6 45.6 7639 2 US-08-232-016-22 Sequence 22, 188 45.2 5864 3 US-08-894-44 Sequence 4, 188 45.2 5864 3 US-09-458-093-4 Sequence 24, 179 43.0 1077 4 US-09-458-0378-24 Sequence 24,	ď	ę.	45.6	86	4	09-430-497A	H
189.6 45.6 7639 2 US-08-232-016-22 Sequence 22. 188 45.2 5864 3 US-08-894-440-4 Sequence 4, 18 45.2 5864 3 US-09-458-093-4 Sequence 4, 179 43.0 1077 4 US-09-4557-037B-24 Sequence 24,	_	e,	45.6	56	7	-08-232-016-	23
188 45.2 5864 3 US-08-894-440-4 Sequence 4, 188 45.2 5864 3 US-09-458-093-4 Sequence 24, 179 43.0 10.77 4 US-09-457-037B-24 Sequence 24,	===	ď,	45.6	63	~	-08-232-016-2	22,
188 45.2 5864 3 US-09-458-093-4 Sequence 4, 179 43.0 1077 4 US-09-457-037B-24 Sequence 24,		188	45.2	86	m	-08-894-440-	4
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Sequence 2	Sequence 2	Seguence 2	Sequence 4	Sequence 4	Sequence 4	Seguence 2	Sequence 2	Sequence 2	Sequence 2	Seguence 7	Sequence 3	Seguence 3	Sequence 2	Sequence 2	Sequence 5	Sequence 5	Sequence 4
US-09-733-151-24	US-08-453-104-22	US-08-694-824-22	US-09-847-057-4	US-09-874-926-4	US-09-948-138-4	US-08-064-121-2	US-08-478-015-2	US-08-475-975-2	US-09-084-889-2	US-09-794-384A-7	US-09-080-625-3	US-09-695-782-3	US-09-080-625-2	US-09-695-782-2	US-09-080-625-5	US-09-695-782-5	US-09-080-625-4
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1077	3201	3201	8340	8340	12241	1186	1186	1186	1186	831	3153	3153	3336	3336	3694	3694	3877
43.0	42.5	42.5	37.2	37.2	37.2	36.7	36.7	36.7	36.7	35.0	35.0	35.0	35.0	35.0	.35.0	35.0	35.0
179	176.6	176.6	154.6	154.6	154.6	152.6	152.6	152.6	152.6	145.6	145.6	145.6	145.6	145.6	145.6	145.6	145.6
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ALIGNMENTS

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NAME/KEY: misc feature
LOCATION: Complement((5840)..(5864))
                                           US-08-894-440-4
360
                                                                                          301 AIGTACATATATTATATGAACATGATTAATGCTTGTGAGTTGTTCTCTTCGTAAGAGT 360
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                                                                                                                                                                                                                      TTGCTTGGACTATAATACCTGACTTGTTATTTTTTATCAATAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 CCCCIGCTGCTTTACATGGATTTCTTCGCTACTATTCTATACGTGTATATACGCTAT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 AATGTACATATATTATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAG 359
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                                                       AIGTACATATATATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAGT
                                                                                                                             361 TTCAATATGTAATGGTGAAGAGTCAAAACCCAAAATCATGAACACCCAAACTCGAT 416
                                                                                                                                                     295 TATTTAAACTATATTTCTTTCAAGAAATTAACATCTACAAATTGCCTTTTCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AATGTACATATATATATGAACATGATTAATGCTTGTGAGTTGTTCTCATCCGTAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GACCATGTACATCCTACCATAATTATAATTATAATTATAATAC-TGAAACCATGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: 5' border OTHER INFORMATION: flanking region of elite event MS-B2
NAME/KEY misc_feature
LOCATION: (1)..(234)
OTHER INFORMATION: plant DNA
NAME/KEY misc_feature
LOCATION: (235)..(415)
OTHER INFORMATION: T-DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 TITCAATATGTAATGGTGAAGAGTCAAAACCCCAAAATCATGAACACCCAA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.5%; Score 380.8; DB 4; Length 415; 98.5%; Pred. No. 6.7e-85; live 1; Mismatches 3; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITCAATATGTAATGGTGAAGAGTCAAAAACCCAAAATCATGAACACCAAA 7
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/430,497A;
CURRENT APPLICATION NUMBER: US/09/430,497A;
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
TYPET 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCAATAAAWITATGTT
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Best Local Similarity 98.5
Matches 404; Conservative
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                                                       301
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FEATURE:
NAME/KRY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113 FEATURE:
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LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAME/KEY: misc feature
LOCATION: Complement((331)..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
Sequence 4, Application US/08894440

Patent No. 6025546

GENERAL INFORMATION:

APPLICANT: FLANT GENETIC SYSTEMS N.V.

ITILE OF INVENTION: Method to obtain male sterile plants

FILE REFERENCE: NMSCOR

CURRENT APPLICATION NUMBER: US/08/894,440

CURRENT APPLICATION NUMBER: US/08/894,440

NUMBER OF SEQ ID NOS: 4

SOUTHARE: PatentIn Ver. 2.0

SEQ ID NOS: 4

LENGTH: 5864
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LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
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NAME/KEX: misc_feature
LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
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LOCATION: (4924).,(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Fnos)
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5620 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 5679
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                                                                                                                                                                                                            1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC 60
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NAME/KEY: misc feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
NAME/KEY: misc feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3/97)
                                                                                                                                                     Gaps
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LOCATION: Complement((1386)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
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LOCATION: Complement((2569)..(3011))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
                                                                                    Query Match 46.3%; Score 192.6; DB 3; Length 5864; Best Local Similarity 99.5%; Pred. No. 2.2e-38; Matches 192; Conservative 1; Mismatches 0; Indels 0;
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LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pssu)
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APPLICANT: PLANT GENETIC SYSTEMS N.V.
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NAGORE: US/09/458,093
CURRENT APPLICATION NUMBER: US/09/458,093
PRIOR APPLICATION NUMBER: 08/894,440
PRIOR APPLICATION DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN UNE: 2.0
OTHER INFORMATION: left border of Agrobacterium T-DNA
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LOCATION: Complement((331)..(882))
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Sequence 4, Application US/09458093
Patent No. 6344602
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LENGTH: 5864
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US-08-894-440-4
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; NAME/KEY: misc feature
; LOCATION: (4924)..(5216)
; OTHER INPORMATION: promoter of nopaline synthase gene of
; OTHER INPORMATION: Agrobacterium T-DNA (Pnos)
; NAME/KEY: misc_feature
; LOCATION: (5217)..(5490)
; OTHER INPORMATION: amyloliquefaciens
; OTHER INPORMATION: region coding for barstar of Bacillus
; OTHER INPORMATION: cequine
; OTHER INFORMATION: region containing polyadenylation signal of gene 7
; OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
; NAME/KEY: misc_feature
; LOCATION: Complement(5840)..(5864))
; OTHER INFORMATION: left border of Agrobacterium T-DNA
US-09-458-093-4
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APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: SAME
FILE REPRESINCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 5865
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46.3%; Score 192.6; DB 4; Length !

Best Local Similarity 99.5%; Pred. No. 2.2e-38;

Matches 192; Conservative 1; Mismatches 0; Indels
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6471 TATTTAAACTATATTTCTTTCAAGATGGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
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                                    121 TATITTAAACTATAITICTTTCAAGAIGGGAATTAACAICTACAAATIGCCTTTTCTIATC 180
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CTHER INFORMATION: 3'97: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
MAME/KEX: misc_feature
LOCATION: (4336)..(5170)
OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         egion containing the
the nopaline synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR THE REPREBURE: 2.121-0127P
CURRENT APPLICATION WINERE, US/08/817,188
CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER PILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER APPLICATION NUMBER: EP 95401844.6
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: PATENTIN VET. 2.0
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: Complement((5711)..(6262))
COTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
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LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
FEATURE:
FEATURE:
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PB1: promoter region of El gene of
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LOCATION: Complement((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region
OTHER INFORMATION: polyadenylation signal of the
OTHER INFORMATION: gene of Agrobacterium T-DNA.
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45.7%; Score 190; DB 3; L.
Best Local Similarity 99.0%; Pred. No. 9.9e-38;
Matches 190; Conservative 1; Mismatches 1;
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Parcht No. 6074875
GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
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LENGTH: 6548
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                                                5741 TAITTAAACIATATTICTITICAAGAIGGGAATTAACAICTACAAATIGCCITITICTIAIC 5800
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TATTIAAACTATATTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
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NAME/KEY: misc feature
NAME/KEY: misc feature
OCCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER_INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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NAME/KEY: misc_feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.7%; Score 190; DB 3; Length 6548; Best Local Similarity 99.0%; Pred. No. 9.9e-38; Matches 190; Conservative 1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
LOCATION: (5711). (6262)
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                             Sequence 1, Application US/08894440

Patent No. 6025546;

GENERAL INFORMATION:

APPLICANT: PLANT GENETIC SYSTEMS N.V.

TITLE OF INVENTION: Method to obtain male sterile plants;

FILE REPERENCE: NNSCOR

CURRENT APPLICATION NUMBER: US/08/894,440;

CURRENT FILING DATE: 1997-11-12;

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (vector)
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NAME/KEY: misc feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
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NAME/KEY: misc feature
LOCATION: Complement ((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El
OTHER INFORMATION: (PEl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1). (2003)
OTHER INFORMATION: pUC19 derived vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                             5801 GACCATGTACATC 5813
                                                                                                        181 GACCATGTACATC 193
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NAME/KEY: misc feature
LOCATION: (1)...(2003)
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US-08-894-440-1
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6471 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 6530
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LOCATION: 484..684..684
COTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of I-DNA gene 7"
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APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CORNELISSEN, MARCUS
APPLICANT: CORNELISSEN, MARCUS
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: WARSSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES: 6
CORRESSEDNUBRUE ADDRESS:
ADDRESSEDE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DESCRIPT: PC-DOS/MS-DOS/COMPUTER: PC-DOS/MS-DOS/COMPUTER: PC-DOS/MS-DOS/COMPUTER: PC-DOS/MS-DOS/COMPUTER: PC-DOS/MS-DOS/COMPUTER: PC-DOS/MS-DO
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LOCATION: 194..718
OTHER INFORMATION: /note= "T-DNA right border"
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LOCATION: complement (729..1340)
LOCATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
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NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
FEATURE:
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LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
FBATURE:
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NAME: SVENSEON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECHONIS: (703) 205-8000
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                        US-08-549-680A-5/c
; Sequence 5, Application US/08549680A
; Patent No. 5962768
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INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYBE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                    6531 GACCATGTACGT 6542
                                                                                                                     181 GACCATGTACAT 192
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TELEX: 2
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                  61 ATCAATAAAWTTATGTTTTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
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LOCATION: (5711)...(6262)

OTHER INFORMATION: region coding for phosphinothricin acetyl

OTHER INFORMATION: transferase (bar)

NAME/KEY: misc_feature

LOCATION: (6263)...(6496)

OTHER INFORMATION: region containing polyadenylation signal fo gene 7

OTHER INFORMATION: of Agrobacterium T-DNA (3/g7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
NAME/KEY: misc_feature
LOCATION: (1). (2003)
OTHER INFORMATION: pUC19 derived vector sequences (vector)
NAME/KEY: misc_feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: argion coding for barnase of Bacillus
OTHER INFORMATION: argioliquefaciens
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice
OTHER INFORMATION: (PE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
UNTER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
NAME/KEY: misc_feature
LOCATION: (571I)..(6262)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09458093
; Sequence 1, Application US/09458093
; Patent No. 6344602
; GENERAL INFORMATION:
    APPLICANT: PLANT GENETIC SYSTEMS N.V.
    TITLE OF INVENTION: Method to obtain male sterile plants
; FILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/09/458,093
; CURRENT PILING DATE: 1999-12-10
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; MENTH: 6548
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Best Local Similarity 99.0%; Pred. No. 9.9e-38;
Matches 190; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           6531 GACCATGTACGT 6542
                                                                                                                                                                                                                                                                         181 GACCATGIACAT 192
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US-09-458-093-1
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fragment of pTS88
OTHER INFORMATION: fragment of pTS88
OTHER INFORMATION: fragment of pTS88
INCORPATION: (1) - (35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
OTHER INFORMATION: (2694)
OTHER INFORMATION: CM1841 (P355)
OTHER INFORMATION: CM1841 (P355)
OTHER INFORMATION: cM1841 (P355)
OTHER INFORMATION: cm1841 (P355)
OTHER INFORMATION: cm2010 coding for barstar of Bacillus
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: region coding for barstar of Bacillus
                                                                                                                                                TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
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         Gaps
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LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fequence 2, Application US/09458093
Fatent No. 6344602
GENERAL INFORMATION:
FILE OF INVENTION:
FILE OF INVENTION: Method to obtain male sterile plants
FILE REPRENCE: NMSCOR
CURRENT PLING DATE: 1999-12-10
FRIOR PELING DATE: 1999-12-10
FRIOR PRING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2.
         Indels
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         0;
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45.6%; Score 189.6; DB 3;
Best Local Similarity 99.5%; Pred. No. 8.7e-38;
Matches 189; Conservative 1; Mismatches 0;
       Mismatches
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OTHER INFORMATION: polylinker of pGEM2
         Ξ,
       Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  1278 GACCATGTAC 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 TATTTAAACTATATTTTTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTTCTTATC 450
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                                                                                                                                                                                                                                                                               629 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
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                                                                                                                                                                                             Gaps
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OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI
OTHER INFORMATION: fragment of pTS88
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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MAMBE/KEY: misc feature

LOCATION: (36) - (694)

OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus strain

OTHER INFORMATION: CM1841 (P35S)
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (968)...(1287)
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.6%; Score 189.6; DB 3; Length 1303; 99.5%; Pred. No. 8.7e-38;
                                                                                                                                        Query Match 45.7%; Score 190; DB 2; Length 7811; Best Local Similarity 99.0%; Pred. No. 1e-37; Matches 190; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 2.7 Application US/08894440 |
| Patent No. 6025546 |
| GENERAL INPORMATION: GENETIC SYSTEMS N.V. |
| TITLE OF INVENTION: Method to obtain male sterile plants |
| FILE REFERENCE: NMSCOR |
| CURRENT APPLICATION UNMBER: US/08/894,440 |
| CURRENT FILING DATE: 1997-11-12 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTMARE: Patentin Ver. 2.0 |
| SEQ ID NO 2 |
| LENGTH: 1303
                                                                                                                                                                                          1; Indels
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NAME/KEY: misc feature
LOCATION: (6957...(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: 3001..302.
LOCATION: 3001..302.
CHER INFORMATION: Sequences"
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LOCATION: (1). (35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
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LOCATION: (1288)...(1303)
OTHER INFORMATION: polylinker of pGEM2
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                                                                                                                                                                                                                                                                                                                                 61 ATCAATAAAWITAIGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GACCATGTACAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 GACCATGTACGT 438
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Best Local Similarity
                                                                                            US-08-549-680A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-894-440-2
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Sequence 23, Application US/08694824
Sequence 23, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
APPLICANT: SOUTHLISSEN, Marc
APPLICANT: SOUTHLISSEN, Marc
APPLICANT: STAM, Maike
APPLICANT: TAM, Maike
APPLICANT: DIAM, Maike
APPLICANT: STAM, Maike
APPLICANT: TAM, Maike
APPLICANT: DIAM, Maike
APPLICANT: NOIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                           121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC
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Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts. CITY: Alexandria STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pacpy disk
COMPUTER: Pacpy disk
COMPUTER: Pacpy disk
COMPUTER: Pacpille
COMPUTER: Pacp
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LOCATION: 2078-12082
OTHER INFORMATION: \(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\)\(\note=\}\(\note=\)\(\note=\}\(\note=\)\(\note=\}\(\note=\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\)\(\note=\}\(\note=\}\(\note=\}\(\note=\}\)\(\
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COUNTRY: United States
ZIP: 22313-1404
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EDNESS: single
                                                                                                                                                                                                                                                                                                                       181 GACCATGIAC 190
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US-08-105-104-105-25
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                     1218 TATITAAACTATATTTCTTTCAAGAATTAACATCTACAAATTGCCTTTTCTTATG 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTACGGCAATGTACCAGCTGATATAATCAGTTATTGAAATATTTCTGAATTTAAACTTGC
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45.6%; Score 189.6; DB 1; Length 3200;
Best Local Similarity 99.5%; Pred. No. 1.1e-37;
Matches 189; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: /note= "Nucleotides 2078-2082;
CTHER INFORMATION: wherein N is not known."
US-08-453-104-23
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                                                                                                                                                                                                                                                                                                  1278 GACCATGTAC 1287
                                                                                                                                                                                            181 GACCATGIAC 190
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US-08-453-104-23
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Search completed: December 5, 2004, 07:17:52 Job time : 69.888 secs
      1999-12-08
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PRIOR FILING DATE: 19:
NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin vei;
SEQ ID NO 2
LENGTH: 4832
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                                                                                                                                            FEATURE:
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US-09-733-151-2/C
US-09-733-151-2/C
; Sequence 2, Application US/09733151
; Sequence 2, Application US/09733151
; Sequence 2, Application US/09733151
; Patent No. 6563026
; GENERAL INFORMATION:
; APPLICANT: De Both, et al.
; TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
; FILE REPERENCE: 514412-2019
; CURRENT APPLICATION NUMBER: US/09/733,151
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 09/457,037
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: De BOCH, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR PLING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 4832
                                         3012 AICATAAATTTATGTTTTTGCTTGGACTATAATACCTGACTTGTTATTTTATCATAAA 3071
                                                                                                                     3072 TATTIAAACTATATICTITCAAGAIGGGAATTAACAICTACAAAITGCCTITITCTIAIC 3131
                       TTTGCTTGGACTATAATACCTGACTTGTTATTTTATCAATAAA 120
                                                                                              121 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 180
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Pred. No. 1.2e-37;
1; Mismatches 0; Indels 0;
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CTHER INFORMATION: T-DNA of Plasmid pTHW118
NAME/KRY: misc feature
LOCATION: (1883)..(4065)
COTHER INFORMATION: Hpa I restriction fragment
US-09-457-037B-2
                                                                                                                                                                                                                                                                        RESULT 14
US-09-457-037B-2/c
; Sequence 2, Application US/09457037B
; Betten No. 6506963
; GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 189; Conservative
                  ATCAATAAAWTTATGT1
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61 AICAATAAAWITAIGITITIGGITIGGACTATAATACCIGACTIGITAITTAICAATAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 TATTTAAACTATATTTCTTTCAAGATGGGAATTAACATCTACAAATTGCCTTTTCTTATC 64
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Best Local Similarity 99.5%; Pred. No. 1.2e-37;
Matches 189; Conservative 1; Mismatches 0;
                                                                                                                                                                   NAME/KEY: misc_feature
DCCATION: (1)..(4832)
CTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
PatentIn version 3.0
                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 8, Application US/09430497A
Patent No. 6509516
GENERAL INFORMATION:
APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: SAME
FILE REFERENCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT APPLICATION NUMBER: US/09/430,497A
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GIATATATACACGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGCAGCAGGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHER INFORMATION: Description of Artificial Sequence: 5' border OTHER INFORMATION: flanking region of elite event MS-B2 MAME/KEY: misc_feature LOCATION: (1). (234) OTHER INFORMATION: plant DNA OTHER INFORMATION: plant DNA MAME/KEY: misc_feature LOCATION: (235). (415). (415). (415). OTHER INFORMATION: T-DNA
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100.0%; Score 415; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.2e-92;
Matches 415; Conservative 0; Mismatches 0;
US-09-733-151-24
US-08-453-104-22
US-09-847-057-4
US-09-948-121-2
US-09-948-1131-2
US-09-948-1131-2
US-08-064-1121-2
US-08-064-1121-2
US-08-08-118-2
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LENGTH: 415
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                            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-430-497A-1

US-08-894-1440-1

US-08-817-440-2

US-08-458-093-1

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US-09-458-093-2

US-09-458-093-2

US-08-457-037B-1

US-09-733-151-2

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Listing first 45 summaries
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                                                                                                       using
                                                                                                                                                2004,
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301 TGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGATGCAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 TATACACGTATACAAATAGTAGCGGAGAAATCCATGTAAAGCAGCAGGGGGCACCATGGT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 TGAGAACAACTCACAAGCATTAATCATGTTCATATAATATATGTACATTATAC-GTATA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 TGAGAACAACTCACAAGCATTAATCATGTTCATATAAATATGTACATTATACGGTATA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCATITICIAGAIGITAATICCCCAICTIGAAAGAATATAGATITAAATATIGATA 111
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: AMAE
FILE REFERENCE: 514412-2020
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 1199-10-29
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATACACGTATACAAATAGTAGCGAAGAAATCCATGTAAAGCAGCAGGGGGCACCATGGT 185
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                                                              TGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAAATTTGATGCAAG
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                                                                                                                                              361 ITTAAATICAGAAATATICAAATAACIGATTATATCAGCTGGTACATTGCCGTAG 415
                                                                                                                                                                           361 TITAAATICAGAAATATITCAATAACTGATIATATATCAGCTGGTACATIGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: 3' border OTHER INFORMATION: flanking region of elite event MS-B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 380.8; DB 4; Length 416;
Pred. No. 8.4e-84;
1; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTCAGABATATTTCABTABACTGATTATATCAGCTGGTACATTGCCGTAG 1
                                                                                                                                                                                                                                                  RESULT 2
US-09-430-497A-10/c
YE-09-610, Application US/09430497A
Patent No. 6509516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.5%;
Matches 404; Conservative
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LOCATION: (194)...(416)
OTHER INFORMATION: plant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1)...(193)
OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-430-497A-10
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                                                              301
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LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
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LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COCATION: (5490)..(5765)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: nopaline synthase gene of Agrobacterium T-DNA
OTHER INFORMATION: (3'nos)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: T-DNA of OTHER INFORMATION: plasmid pTCO113
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LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco
OTHER INFORMATION: Arabidopsis (Pssu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: Complement((331),..(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
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LOCATION: (5217)..(5489)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: region coding for barnase of Bacillus OTHER INFORMATION: amyloliquefaciens
                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PLANT GENERIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPERENCE: NMSCOR
FILE APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 5864
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NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA
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LOCATION: (4924)..(5216)
OTHER INFORMATION: promoter of nopaline synthase gene
OTHER INFORMATION: Agrobacterium T-DNA (Pnos)
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LOCATION: Complement((3032)..(3367))
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Complement((5840)..(5864))
US-08-894-440-4/c
; Sequence 4, Application US/08894440
; Patent No. 6025546
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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NAME/KEY: misc feature
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                                                                                                                                                                 TATAGITIAAATAITITATIGATAAAATAACAAGICAGGIATIATAGICCAAGCAAAAACA 342
                                                                                                                                                                                                                                                                                                                                                             TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGG 402
                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((3032)..(3367))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: Complement((3368)..(4877))
OTHER INFORMATION: promoter of stamen-specific TA29 gene of Nicotiana
OTHER INFORMATION: tabacum (PTA29)
                                                                                                                      Gaps
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LOCATION: Complement((883)..(2608))
OTHER INFORMATION: promoter of small subunit gene of Rubisco of
OTHER INFORMATION: Arabidopsis (Pseu)
NAME/KEY: misc_feature
LOCATION: Complement((2659)..(3031))
OTHER INFORMATION: region containing polyadenylation signal of
OTHER INFORMATION: (3'nos)
                                                                 Score 191.4; DB 3; Length 5864; Pred. No. 1.4e-37; 0; Mismatches 1; Indels 0;
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NAME/KEY: misc feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: right border of Agrobacterium T-DNA (RB)
NAME/KEY: misc feature
LOCATION: Complement((98)..(330))
OTHER INFORMATION: region containing polyadenylation signal of OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
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LOCATION: Complement (1311)...(882))
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
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APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION:
FILE OF INVENTION: Method to obtain male sterile plants;
FILE REFERENCE: NASCOR
CURRENT APPLICATION NUMBER: US/09/458,093
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 08/894,440
PRIOR APPLICATION NUMBER: 08/894,440
NUMBER OF SEQ ID NOS: 4-11-12
NUMBER OF SEQ ID NOS: 4-11-12
SEQ ID NOS: 4-11-12
SEQ ID NOS: 4-140
; OTHER INFORMATION: left border of Agrobacterium T-DNA US-08-894-440-4
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Patent No. 6344602
                                                                    46.1%;
99.5%;
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                                                                    Query Match
Best Local Similarity 99.5
Matches 192; Conservative
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US-09-458-093-4/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 TATAGTITAAATATITATIGATAAAATAACAAGICAGGTATITATAGICCAAGCAAAAACA 342
  COCATION: (4924). (5216)
COTHER INFORMATION: promoter of nopaline synthase gene of
COTHER INFORMATION: promoter of nopaline synthase gene of
COTHER INFORMATION: Agrobacterium T-DNA (Phos)
NAME/KEY: misc feature
COTHER INFORMATION: region coding for barstar of Bacillus
COTHER INFORMATION: amyloliquefaciens
COTHER INFORMATION: region containing polyadenylation signal of gene
COCATION: (5490)...(5765)
COTHER INFORMATION: of Agrobacterium T-DNA (3'97)
NAME/KEY: misc feature
LOCATION: Complement((5840)..(5864))
COTHER INFORMATION: left border of Agrobacterium T-DNA
COTHER INFORMATION: left border of Agrobacterium T-DNA
COTHER INFORMATION: left border of Agrobacterium T-DNA
US-09-458-093-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WESTON, Brigitte
APPLICANT: WESTON, Brigitte
APPLICANT: DE BEUCKELEER, Marc
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS AND METHOD FOR PRODUCING
TITLE OF INVENTION: MALE-STERILE BRASSICA PLANTS
CURRENT APPLICATION NUMBER: US/09/430,497A
CURRENT FILIAG DATE: 1999-10-29
SUPPRENT FILIAG DATE: 1999-10-29
SOFTWARE: PATENTIN US: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-09-430-497A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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46.1%; Score 191.4; DB 4;
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
46.1%; Score 191.4; DB 3
Best Local Similarity 99.5%; Pred. No. 1.4e-37;
Matches 192; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-430-497A-1/c
; Sequence 1, Application US/09430497A
; Patent No. 6509516
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5632 TACATTGCCGTAG 5620
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feature
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LENGTH: 5865
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6422 AAAITTATIGATGCAAGITTAAAITCAGAAATATITCAAIAACIGAITAIAITCAGCIGGI 6363
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                                344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT
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                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08817188;
Sequence 2, Application US/08817188;
Patent No. 6074876;
GENERAL INFORMATION:
APPLICANT: DE BLOCK, MARC
TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR;
FILE REPERENCE: 2121-0127P;
CURRENT APPLICATION NUMBER: US/08/817,188;
CURRENT FILING DATE: 1997-05-15
BARLIER FILING DATE: 1996-07-31
BARLIER FILING DATE: 1996-07-31
BARLIER FILING DATE: 1996-07-31
SACHMARE: RAPPLICATION NUMBER: EP 95401844.6
BARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 5
SOFTMARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc.feature; LOCATION: (6263)..(6496); OTHER INFORMATION: 3'g7: 3' untranslated region containing the OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium; OTHER INFORMATION: T-DNA US-08-817-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement ((2019)..(2288))
OTHER INFORMATION: 3' nos: 3' untranslated region containing the
OTHER INFORMATION: polyadenylation signal of the nopaline synthase
OTHER INFORMATION: gene of Agrobacterium T-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4336)..(5170)
CTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic
OTHER INFORMATION: Virus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: Complement((5711)..(6262))
OTHER INFORMATION: bar: region coding for phosphinotricin
OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: PEl: promoter region of El gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAMEN FREY: misc_feature
NAMEN FREY: misc_feature
LOCATION: Complement((2289)..(2624))
OTHER INFORMATION: barnase: region coding for barnase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                    6362 ACATTGCCGTAG 6351
                                                                                                                                      404 ACATTGCCGTAG 415
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                                                                                                                                                                                                                                                                                                   US-08-817-188-2/c
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Best Local Simi
Matches 190;
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                                5693 TAAATTTATIGAIGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGG 5634
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343 TAAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 ATAGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEX: misc_feature
LOCATION: (6263)..(6496)
OTHER INFORMATION: region containing polyadenylation signal fo gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3'97)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: Complement((2019)..(2283))
OTHER INFORMATION: 3' nos: region containing polyadenylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
COGYION: Complement((12625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice
OTHER INFORMATION: (PEI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (4336)..(5710)
OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 188.8; DB 3; Length 6548;
Pred. No. 6.3e-37;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (5711)..(6262)
OTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (vector)
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NAME/KEY: misc_feature
LOCATION: Complement((2284)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08894440

Patent No. 6025546

CENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REPERENCE: NMSCOR
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LOCATION: (1).7(2003)
OTHER INFORMATION: pUC19 derived vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/894,440
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 99.0%;
Matches 190; Conservative (
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                                                                                                         403 TACATTGCCGTAG 415
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US-08-894-440-1/c
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US-08-894-440-1
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6422 AAATITATTGATGCAAGTITAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 6363
                                                                                                                                               5362 ACATTGCCGTAG 6351
                                                                                           404 ACATTGCCGTAG 415
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NAME/KEY:
LOCATION:
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           6482 ATAGITTABARTATITATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACAT 6423
                                                                                                                              6422 AAATITATIGATGCAAGITITAAAITICAGAAATATITCAATAACIGAITATATATGGGT 6363
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                                                                                                 344 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 403
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LOCATION: (4336)..(5710)
COTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)
COTHER INFORMATION: 16620)
COTHER INFORMATION: region coding for phosphinothricin acetyl
OTHER INFORMATION: transferase (bar)
NAME/KEY: misc feature
LOCATION: (6263)..(6496)
COTHER INFORMATION: region containing polyadenylation signal fo gene 7
COTHER INFORMATION: of Agrobacterium T-DNA (3'97)
US-09-458-093-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: COMPLEMENT((2019)..(2283))
OTHER INFORMATION: Of nos: region containing polyademylation signal
OTHER INFORMATION: of nopaline synthase gene of Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: Complement((2244)..(2624))
OTHER INFORMATION: region coding for barnase of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: Complement((2625)..(4313))
LOCATION: Complement((2625)..(4313))
OTHER INFORMATION: promoter of the stamen-specific El gene of rice
OTHER INFORMATION: (PE1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.5%; Score 188.8; DB 3; Length 6548; 99.0%; Pred. No. 6.3e-37; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09458093
; Sequence 1, Application US/09458093
; Sequence 1, Application US/09458093
; GENERAL INFORMATION:
APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants;
FILE REFERENCE: UNSCOR
; CURRENT PILING DATE: 1999-12-10
; RIOR APPLICATION NUMBER: 08/894,440
; PRIOR PILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTMARE: Patentin Ver. 2.0
; SEQ ID NO :
LENGTH: 6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (1). (2003)
OTHER INFORMATION: pUC19 derived vector sequences (vector)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                         6362 ACATTGCCGTAG 6351
                                                                                                                                                                                                        404 ACATTGCCGTAG 415
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Best Local Similarity
Matches 190; Conserva
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NAME/KEY: misc_feature
LOCATION: 484..684..60
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
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APPLICATION NUMBER: US/08/549,680A
FILLING DATE: 16 JANUARY 1996
CLASSIFICATION: 600
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REGISTRATION NUMBER: 3121-0111P
TELECHMONICATION INFORMATION:
TELECHMONE: (703) 205-8000
                                                                            APPLICANT: CORNELISSEN, MARCUS
APPLICANT: REYNABRIS, ARLETTE
APPLICANT: GOSSELE, VERONIQUE
APPLICANT: VAN AARSEN, ROEL
TITLE OF INVENTION: MARKER GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector pTRVA3
FERVURE:
NAME/KEY: misc_feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
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LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8000
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
TYPE: TELETATERISTICS:
TYPE: DANG (Synthetic)
FEATURE:
Sequence 5, Application US/08549680A Patent No. 5962768 GENERAL INFORMATION:
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Matches 189; Conservative
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                                                                                                                                                                                                                                                                           406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-458-093-2/c
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                                                                                                                                                                                                                                                                                                                                                                               558 AAATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGT 617
                                                                                                                                                                                                 284 ATAGITITAAATATITATIGATAAAATAACAAGICAGGIATIATAGICCAAGCAAAAAAT 343
                                                                                                                                                                                                                                                                                                                   498 ATAGTTTAAATATTTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAAACAT 557
                                                                                                                                                                                                                                                                                                                                                        344 AAATTTATTGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATATCAGCTGGT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene 7
OTHER INFORMATION: of Agrobacterium T-DNA (3.g7)
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: HindIII-ECORI OTHER INFORMATION: fragment of pTS88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (36)...(694)
COTHER INFORMATION: 358 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (P35S)
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                                                                                                                  Length 7811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-08-944-40-2/c
US-08-994-440-2/c
; Sequence 2, Application US/08894440
; Patent No. 602546
; General No. 602546
; GENERAL INFORMATION:
; TITLE OF INVENTION: Method to obtain male sterile plants
; TILE REFERENCE: NMSCOR
; CURRENT APPLICATION NUMBER: US/08/894,440
; CURRENT FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 2
                                                                                                                  Score 188.8; DB 2; Length Pred. No. 6.6e-37; O; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: CM1841 (P35S)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (695)..(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
NAME/KEY: misc_feature
LOCATION: 3001..3023
LOCATION: 3001..3023
OTHER INFORMATION: sequences"
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NAME/FEX: misc_feature
NOCATION: (1)._(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
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LOCATION: (1288).. (1303)
CHER INFORMATION: polylinker of pGEM2
US-08-894-440-2
                                                                                                                ASST FACTOR SIMILARITY 99.0%;
Matches 190; Conservative C
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618 ACATTGCCGTAG 629
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Best Local Similarity
                                                              ; OTHER INFC
US-08-549-680A-5
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1167 ATTTATTGATGATGTTTAAATTCAGAAATATTTCAATAACTGATTATATATGATGGTAC 1108
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                                                                                                                                                                         286 AGTTTAAATATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA
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Gaps
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NAME/KBY: misc_feature
LOCATION: (1)...(35)
OTHER INFORMATION: polylinker of pGEM2 (pGEM2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (968)..(1287)
OTHER INFORMATION: region containing polyadenylation signal of gene
OTHER INFORMATION: of Agrobacterium T-DNA (3'g7)
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (36)...(694)
OTHER INFORMATION: 3158 promoter of Cauliflower Mosaic Virus strain
OTHER INFORMATION: CM1841 (F35S)
NAME/KEY: misc_feature
LOCATION: (695)...(967)
OTHER INFORMATION: region coding for barstar of Bacillus
OTHER INFORMATION: amyloliquefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09458093

Patent No. 6344602
GENERAL INFORMATION:
FILE APPLICANT: PLANT GENERIC SYSTEMS N.V.
TITLE OF INVENTION: Method to obtain male sterile plants
FILE REFERENCE: NAGOR
CURRENT APPLICATION NUMBER: US/09/458,093
CURRENT APPLICATION NUMBER: US/09/458,093
CURRENT FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 08/694,440
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2.
1; Indels
                                                           226 GTACATGGCCGATAAGAAAAGGCAATTTGTAGATGTTAATTCCCATC
0; Mismatches
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US-09-458-093-2
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ORGANISM: Artificial Sequence
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Sequence 23, Application US/08694824
Patent No. 5877306
GENERAL INFORMATION:
APPLICANT: SCEPARET, Piet
APPLICANT: SCEPARET, Piet
APPLICANT: DOCK, Jan
TITLE OF INVENTION: MODIFIED BACILLUS THURINGIENSIS
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                           3021 ATTTATTGATGCAAGTTTAAAATTCAGAAATATTTCAATAACTGATTATATCAGGTAC 2962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3081 AGTITAAATATITATIGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 3022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Burns, Doane, Swecker & Mathie STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Acavandria George Mason Bldg., Washington & Prince Sts.
CITY: Thexandria George COWTHY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Description of Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
COMPUTER: Description DATA: BC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: BC-0926
FILING DATE: 09-AUG-1996
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 30,427
TELEPHONE: (703) 816-6620
TELEPHONE: (703) 816-6620
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: (703) 836-2021
TELEPHONE: TELEPHO
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OTHER INFORMATION: /note= "Nucleotides 2078-2082
OTHER INFORMATION: wherein N is not known."
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LOCATION: 2078..2082
                                                                                                                                                                                                                                          2961 ATTGCCGTAG 2952
                                                                                                                                                                                              406 ATTGCCGTAG 415
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STRANDEDNESS: sing
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Best Local Similarity
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Patent No. 5633446

GENERAL INFORMATION:
APPLICANT: SOETAERT, Piet
APPLICANT: SOETAERT, Piet
APPLICANT: DOCKX, Jan
TITLE OF INVENTION: INSECTICIDAL - CRYSTAL PROTEIN GENES AND THEIR EXPRESSION
TITLE OF INVENTION: IN PLANT CELLS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
1167 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STARET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STARE: Virginia
COUNTRY: United States
ZIP: Z2313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,104
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: US 07/937,869
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: REA TERES SEQ 100 SS 00
FILING DATE: 10-DEC-1992
APPLICATION NUMBER: 010830-032
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAK: (703) 836-2620
INFORMATION FOR SEQ ID NO: Z3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature;
| IOCATION: 2078...2082
| OTHER INFORMATION: /note= "Nucleotides 2078-2082;
| OTHER INFORMATION: wherein N is not known."
US-08-453-104-23
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Matches 189; Conservative
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STRANDEDNESS: single
                                                                                             406 ATTGCCGTAG 415
                                                                                                                                                                                                                                                       RESULT 12
US-08-453-104-23/c
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                                                                                                                                                                                                                                                                                                           APPLICANT: De Both, et al.

TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE REPERENCE: 5.14412-2019
FILE REPERENCE: 5.14412-2019
CURRENT APPLICATION NUMBER: US/09/457,037B
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
                                                                                         8021 AITTATTGAIGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 2962
                         3081 AGTTTAAATATTTATTGATAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 3022
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AGTTTAAATATTTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAA 345
                                                                   346 ATTTATTGATGCAAGTTTAAATTCAGAAATATTTCAATAACTGATTATATCAGCTGGTAC 405
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US-09-733-151-2
Sequence 2, Application US/09733151
Sequence 2, Application US/09733151
Parent No. 6563026
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT APPLICATION NUMBER: 09/457,037
                                                                                                                                                                                                                                                           Sequence 2, Application US/09457037B Patent No. 6506963 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                        2961 ATTGCCGTAG 2952
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                                                                                                                                                                                                NAME/KEY: misc_feature

| LOCATION: (1)..(4832)

| CTHER INFORMATION: Plasmid pTHW118

US-09-733-151-2
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406 ATTGCCGTAG 415
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Page

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(c) 1993 - 2004 Compugen Ltd.
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US-09-698-903B-8 415 1 gtcgagtttggtgttcatga......cagctggtacattgccgtag 415 3694831 seqs, 2747406616 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table: score: Title: Perfect sc Sequence: Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Published Applications NA:*

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11: /cgn2 6/prodata/2/pubpna/US60_NEW_PUB.seq:*
12: /cgn2 6/prodata/2/pubpna/US60_NEW_PUB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 13, Appl	Sequence 100, App
ΩI	US-10-027-880-5	US-09-509-945-5	US-09-509-945-4	US-09-733-151-2	US-10-375-332-2	US-09-733-151-1	US-10-375-332-1	US-09-970-921-7	US-09-733-151-24	US-10-375-332-24	US-10-047-542-13	US-10-047-542-100
DB	15	σ	σ	6	15	σ	15	σ	σ	15	13	13
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* Query Match	46.1	45.5	45.5	45.4	45.4	45.4	45.4	45.4	43.2	43.2	37.3	37.3
Score	191,4	188.8	188.8	188.4	188.4	188.4	188.4	188.4	179.4	179.4	155	155
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155 5 5 6 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	101 101 97.4 97.4
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ALIGNMENTS

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APPLICANT: HOFFMAN, BEATE
APPLICANT: HOFFMAN, BEATE
TITLE OF INVENTION: PROMOTER EXPRESSED SPECIFICALLY IN PLANT ROOT CELLS,
TITLE OF INVENTION: VECTORS AND RECOMBINANT HOST CELLS CONTAINING SUCH A
TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED
TITLE OF INVENTION: PROMOTER AND TRANSGENIC PLANTS OBTAINED
CURRENT FILE REPERENCE: CHEP: 003105
CURRENT APPLICATION NUMBER: US/10/027,880
CURRENT APPLICATION NUMBER: PCT/FR00/01768
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
LENGTH: 7599
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, OTHER INFORMATION: Description of Artificial Sequence: T-DNA of PGKB5
US-10-027-880-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.5%; Pred. No. 6.6e-30;
Matches 192; Conservative 0; Mismatches 1; Indels 0;
                   Sequence 5, Application US/10027880 Publication No. US20030106105A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
US-10-027-880-5/c
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RESULT.4

US-09-733-151-2

Sequence 2, Application US/09733151

Sequence 2, Application US/09733151

Sequence 2, Application US/09733151

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/733,151

CURRENT PELING DATE: 1999-12-08

SETION APPLICATION NUMBER: 09/457,037

NUMBER OF SEQ ID NOS: 43

SOFTWARRE: Patentin Version 3.0

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10375332
Publication No. US20030188347A1
GENERAL INFORMATION:
APPLICANT: DE BOth, et al.
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
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    Length 6548;
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                                        Indels
Score 188.8; DB 9;
Pred. No. 2.2e-29;
0; Mismatches 2;
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; OTHER INFORMATION: Plasmid pTHW118
US-09-733-151-2
  Query Match
Best Local Similarity 99.0%;
Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Matches 189; Conservative
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US-10-375-332-2
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TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REPERENCE: 023-0148P
CURRENT APPLICATION NUMBER: US/09/509,945
CURRENT FILING DATE: 2001-04-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO S
LENGTH: 6539
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Patent No. US20020166140A1

Patent No. US20020166140A1

APPLICANT: HAMADA, Kazuyuki et al.

TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
FILE REFERENCE: 0230-0148P

CURRENT APPLICATION NUMBER: US/09/509,945

CURRENT FILEM DATE: 2001-04-01

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1
                                              6651 TAAATITATIGATGCAAGTITAAATICAGAAAIATITCAATAACTGATTATATCAGCTGG 6592
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Pred. No. 2.2e-29;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                     US-09-509-945-5/c
Sequence 5, Application US/09509945
Patent No. US20020166140A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature; OTHER INFORMATION: Clone: pTS431
US-09-509-945-5
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; NAME/KEY: misc feature
; OTHER INFORMATION: Clone: pTS172
VS-09-509-945-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Escherichia coli LE392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Escherichia coli LE392
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Best Local Similarity 99.0%;
Matches 190; Conservative (
                                                                                                                                         5591 TACATIGCCGIAG 6579
                                                                                                     TACATTGCCGTAG 415
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US-09-509-945-4/c
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Sequence 1, Application US/10375332

| Sequence 1, Application US/10375332
| Publication No. US2030188347A1
| GENERAL INFORMATION:
| APPLICANT: DE BOCH. |
| TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
| TITLE OF INVENTION: HYBRID WINTER US/10/375,332
| CURRENT APPLICATION NUMBER: US/09/733,151
| PRIOR FILING DATE: 2000-12-08
| PRIOR FILING DATE: 1999-12-08
| NUMBER OF SEQ ID NOS: 43
| SEQ ID NO 1
| SEQ ID NO 1
| LINGTH: 4946
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Best Local Similarity 99.5%; Pred. No. 2.4e-29;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
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| Patent No. US20020133845A1
| GENERAL INFORMATION:
| APPLIANT Frank Michiels et al.
| TITLE OF INVENTION: Improved Barstar Gene
| FILE REFERENCE: 2428-0108P
| CURRENT APPLICATION UNMERR: US/09/970,921
| CURRENT FILING DATE: 2001-10-05
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 7
| LENGTH: 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LOCATION: (1)..(4946); OTHER INFORMATION: Plasmid pTHW107US-10-375-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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US-10-375-332-1
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TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
FILE REPERRNCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 09/457,037
PRIOR APPLICATION NUMBER: 09/457,037
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GIACAIGGCCGAIAAGAAAAGGCAAITIGIAGAIGTIAAITCCCAICTIGAAAGAAAIAI 285
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Best Local Similarity 99.5%; Pred. No. 2.4e-29;
Matches 189; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                          Score 188.4; DB 15; Length
Pred. No. 2.4e-29;
0; Mismatches 1; Indels
    PILE REFERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/10/375,332
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US/09/733,151
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 2000-12-08
PRIOR PILING DATE: 1999-12-08
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 2

, LOCATION: (1). .. (4832)

, OTHER INFORMATION: Plasmid pTHW118
US-10-375-332-2

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; LOCATION: (1)..(4946)
OCHER INFORMATION: Plasmid pTHW107
US-09-733-151-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09733151
Patent No. US20010029620A1
GENERAL INFORMATION:
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Best Local
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US-10-375-332-24
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Sequence 24, Application US/09733151
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME
TITLE REPERENCE: 514412-2019
CURRENT APPLICATION NUMBER: US/09/733,151
CURRENT APPLICATION NUMBER: 09/457,037
PRICE PLING DATE: 1999-12-08
PRICE FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 43
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NAME/KEY: misc feature

LOCATION: Complement((1)..(25))

OTHER INFORMATION: label = RB, "T-DNA right border"

NAME/KEY: misc feature

LOCATION: complement((98)..(331))

OTHER INFORMATION: label = 3'97, "region containing 3' untranslated other infoRMATION: label = 3'97, "region containing 3' untranslated other infoRMATION: each of Agrobacterium T-DNA gene 7"

NAME/KEX: misc feature

LOCATION: Complement((332)..(883))

OTHER INFORMATION: label = bar, "region coding for phosphinthricin other infoRMATION: deature

LOCATION: Complement((884)..(2258))

OTHER INFORMATION: Virus"

NAME/KEY: misc feature

LOCATION: Complement(1996)

OTHER INFORMATION: label = PB15S, "35S promoter of Cauliflower Mosaic OTHER INFORMATION: 1abel = PB1, "promoter of El gene of rice (WO OTHER INFORMATION: 2221)..(3969)

OTHER INFORMATION: 22213956)

OTHER INFORMATION: 22213956)

OTHER INFORMATION: 22213956)

OTHER INFORMATION: 22213956)
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (4246)..(4577)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
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LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*; "improved barstar DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 45.4%; Score 188.4; DB 9;
Best Local Similarity 99.5%; Pred. No. 2.5e-29;
Matches 189; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: Complement ((5325)..(5349))
OTHER INFORMATION: label = LB, "T-DNA left border"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn version 3.0
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SEQ ID NO 24
LENGTH: 1077
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US-09-733-151-24
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Sequence 24, Application US/10375332
| Publication No. US20030188347A1
| GENERAL INFORMATION NO. US20030188347A1
| GENERAL INFORMATION NO. US20030188347A1
| TITLE OF INVENTION: HYBRID WINTER OILSEED RAPE AND METHODS FOR PRODUCING SAME FILE OF THE REFERENCE: 5144124-2019
| CURRENT FILING DATE: 2003-22-27
| FILE APPLICATION NUMBER: US/09/733,151
| PRIOR FILING DATE: 2000-12-08
| PRIOR FILING DATE: 1999-12-08
| NUMBER OF SEQ ID NOS: 43
| SEQ ID NO 24
| LENGTH: 1077
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                                                                       NAME/KEY: misc_feature; LOCATION: (1)..(1077)
COTHER INFORMATION: sequence comprising the 5' flanking region of MS-BN1 US-09-733-151-24
                                                                                                                                                                                                                                                                                                                                      940 ATTTATTGATAAAATAACAAGTCAGGTATTATAGTCCAAGCAAAAACATAAATTTATTGA
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                                                                                                                                                                                                                                                    Gaps
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COTHER INFORMATION: sequence comprising the 5' flanking region of US-10-375-332-24
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0
                                                                                                                                                                                                 Length 1077;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                 Score 179.4; DB 9;
Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                 Query Match
Best Local Similarity 99.4%;
Matches 180; Conservative
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Best Local Similarity 99.4%;
Matches 180; Conservative
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
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GENERAL INFORMATION:

Sequence 100, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WCOPF, KEITH L.

ITILE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

TITLE OF INVENTION: AND BACTERIAL DISEASES

FILE REFERENCE: 030905.0004.CIP1

CURRENT APPLICATION NUMBER: US/10/047,542

PRIOR FILING DATE: 2001-10-26

PRIOR PLING DATE: 2001-04-28

PRIOR PLING DATE: 2000-04-28

PRIOR PLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: Patentin Ver. 2.1
US-10-047-542-13/C

; Sequence 13, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION: O. US20020168367A1
; GENERAL INFORMATION: AMES W.
; APPLICANT: LARRICK, JAMES W.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERAL DISEASES
; FILE REFERENCE: 030905.0004.CIPI;
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR FILING DATE: 2001-04-28
; PRIOR FILING DATE: 2000-04-28
; VWHER OF SEQ ID NOS: 101
; SEQ ID NO 13
; SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 TATTATAGTCCAAGCAAAAAATTAATTGATGCAAGTTTAAATTCAGAAATATTTC 380
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSP-1
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; LOCATION: (2214)..(2215)

; CTHER INFORMATION: a, c, t or g

US-10-047-542-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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NAME/KEY: modified base
LOCATION: (2150)
OTHER INFORMATION: a, c, t
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Matches 155; Conservative
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US-10-047-542-100/c
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Sequence 101, Application US/10047542
; Sequence 101, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
    APPLICANT: LARRICK, JAMES W.
    APPLICANT: WYCOFF, KEITH L.
    TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
    TITLE OF INVENTION: NOVEL IMMUNOACH. SOLD CURRENT APPLICANTION NUMBER: US/10/047,542
    CURRENT FILING DATE: 2001-10-26
    PRIOR APPLICATION NUMBER: PCT/US01/13932
    PRIOR APPLICATION NUMBER: 60/200,298
    PRIOR APPLICATION NUMBER: 60/200,298
    PRIOR FILING DATE: 2000-04-28
    NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 101
    LENGTH: 7129
    MUNDER PARENTED TO NOS: 101
    SEQ ID NO 101
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                                                                                                                                                                                                                Length 6602;
                                                                                                                                                                                                                Query Match 37.3%; Score 155; DB 13; Length 6
Best Local Similarity 100.0%; Pred. No. 2.4e-22;
Matches 155; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:
; OTHER INFORMATION: pGPTV-hpt-ocs-35SJ/SC
US-10-047-542-101
                                                                                                                  Description of Unknown Organism:
pGPTV-kan-ocs-ATR-IgA2
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                                         TYPE: DNA
CRGANISM: Unknown Organism
FEATURE:
CHER INFORMATION: DGPTV-kan
US-10-047-542-100
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US-10-047-542-101
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US-10-047-542-14
SEQ ID NO 100
LENGTH: 660
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Search completed: December 5, 2004, 09:36:21 Job time : 331.103 secs
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Patent No. US20020004943A1
GENERAL INFORMATION:
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A PAGODA PHENOTYPE IN PLAN
FILE REPRENENT: PAGADA
CURRENT APPLICATION NUMBER: US/09/847,057
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
## Publication No. US20020168367A1
| GENERAL INFORMATION:
| APPLICANT: LARRICK, JAMES W. |
| APPLICANT: LARRICK, JAMES W. |
| APPLICANT: WAYCOFF, KEITH L. |
| TITLE OF INVENTION: NOVEL IMMUNADHESINS FOR TREATING AND PREVENTING VIRAL |
| TITLE OF INVENTION: AND BACTERIAL DISEASES |
| FILE REFERENCE: 030905.0004.CIP1 |
| CURRENT APPLICATION NUMBER: US/10/047,542 |
| CURRENT FILING DATE: 2001-04-26 |
| PRIOR PILING DATE: 2001-04-28 |
| PRIOR PILING DATE: 2000-04-28 |
| NUMBER OF SEQ ID NOS: 101 |
| SEQ ID NO 14 |
| LENGTH: 8074 |
| LENGTH: 8074
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANIEM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Expression-type plasmid pBMSP-1spJSC
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; ORGANISM: Binary vector pAGI4002
US-09-847-057-4
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; OTHER INFORMATION: a, c, t or g
US-10-047-542-14
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NAME/KEY: modified_base
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US-09-847-057-4
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6554 TATTATAGTCCAAGCAAAACATAAATTTATTGATGCAAGTTTAAATTCAGAAATATTC 6613
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                                                                                           381 AATAACTGATTATCAGCTGGTACATTGCCGTAG 415
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